

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: February 9, 2003, 18:42:23 : Search time 2626 Seconds
(without alignments)
7270.160 Million cell updates/sec

Title: US-10-060-066-2

Perfect score: 656
Sequence: 1 taigctcaactgcacact.....tgtttttttttttttttttt 656

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

GenEmbl: *
1: gb_ba: *
2: gb_hcg: *
3: gb_ln: *
4: gb_om: *
5: gb_ov: *
6: gb_pat: *
7: gb_ph: *
8: gb_pl: *
9: gb_pr: *
10: gb_ro: *
11: gb_sts: *
12: gb_sy: *
13: gb_un: *
14: gb_vl: *
15: gb_da: *
16: em_fun: *
17: em_hum: *
18: em_ln: *
19: em_mu: *
20: em_om: *
21: em_or: *
22: em_ov: *
23: em_pat: *
24: em_ph: *
25: em_pl: *
26: em_ro: *
27: em_sts: *
28: em_un: *
29: em_vl: *
30: em_hcg_hum: *
31: em_hcg_inv: *
32: em_hcg_other: *
33: em_hcg_mus: *
34: em_hcg_pln: *
35: em_hcg_rod: *
36: em_hcg_mam: *
37: em_hcg_vrt: *
38: em_sy: *
39: em_hcgo_hum: *
40: em_hcgo_mus: *
41: em_hcgo_other: *

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	597.8	90.4	185839	2 AC079557	AC079557 Mus muscu
2	525	80.0	178910	2 AC114434	AC114434 Rattus no
3	387.4	59.1	1380	10 AF361350	AF361350 Mus muscu
4	361.6	55.1	142388	2 AC128446	AC128446 Rattus no
5	297.8	45.4	169997	2 AC008440	AC008440 Homo sapi
6	269.8	41.1	1266	2 AF361346	AF361346 Rattus no
7	236	36.0	190210	2 AC022318	AC022318 Homo sapi
8	232.2	35.4	1386	9 AF361354	AF361354 Homo sapi
9	191.2	29.1	633	9 AF234892	AF234892 Homo sapi
10	171	26.1	1281	9 AF288388	AF288388 Homo sapi
11	158.4	24.1	142388	2 AC128446	AC128446 Rattus no
12	92	14.0	987	5 AY037891	AY037891 Gallus ga
13	86.4	13.2	720	9 HSCACNG1	AF142622 Homo sapi
14	86.4	13.2	984	6 AR165149	AR165149 Sequence
15	86.4	13.2	984	6 AX101260	AX101260 Sequence
16	86.4	13.2	984	10 AF361341	AF361341 Rattus no
17	86.4	13.2	984	10 MMU272045	AJ272045 Mus muscu
18	86.4	13.2	1001	9 AF162692	AF162692 Homo sapi
19	86.4	13.2	3392	9 BC034532	BC034532 Homo sapi
20	86.4	13.2	94538	10 AL645853	AL645853 Mouse DNA
21	86.4	13.2	173126	9 AC005988	AC005988 Homo sapi
22	83.2	12.7	1071	6 AR202726	AR202726 Sequence
23	75.4	11.5	209887	2 AC079424	AC079424 Mus muscu
24	62.8	9.6	58937	2 AC129819	AC129819 Rattus no
25	62.4	9.5	1548	5 AF118819	AF118819 Gallus ga
26	58.6	8.9	125020	9 AF429315	AF429315 Homo sapi
27	54.6	8.3	126667	2 AC015839	AC015839 Homo sapi
28	54.4	8.3	972	9 AF096322	AF096322 Homo sapi
29	54.4	8.3	99497	9 HS293166	AL049749 Human DNA
30	53.6	8.2	948	10 AF361340	AF361340 Rattus no
31	53.6	8.2	948	10 MMU272044	AJ272044 Mus muscu
32	53.6	8.2	1477	6 AR202725	AR202725 Sequence
33	53.6	8.2	130440	2 AC130391	AC130391 Rattus no
34	53.6	8.2	187780	2 AC094178	AC094178 Rattus no
35	53.2	8.1	63082	2 AC022663	AC022663 Homo sapi
36	52.8	8.0	972	10 AF361339	AF361339 Rattus no
37	52.8	8.0	1124	10 AF118818	AF118818 Rattus no
38	52.8	8.0	1554	10 AF077739	AF077739 Mus muscu
39	52.8	8.0	1558	6 AR202724	AR202724 Sequence
40	52.8	8.0	155833	2 AC120678	AC120678 Rattus no
41	52.8	8.0	197660	10 AL589650	AL589650 Mouse DNA
42	52.8	8.0	208651	10 AC090493	AC090493 Genomic s
43	52	7.9	948	9 AF100346	AF100346 Homo sapi
44	52	7.9	1012	9 AF134640	AF134640 Homo sapi
45	52	7.9	2092	9 AK054543	AK054543 Homo sapi

ALIGNMENTS

RESULT 1
AC079557 185839 bp DNA linear HTG 02-SEP-2000
LOCUS AC079557
DEFINITION Mus musculus clone RP23-449F12, WORKING DRAFT SEQUENCE, 16
unordered pieces.
ACCESSION AC079557
VERSION AC079557.1 GI:9964922
KEYWORDS HTG, HTGS, PHASE1, HTGS_DRAFT.
SOURCE Mus musculus.
ORGANISM Mus musculus.
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 185839)
AUTHORS DOE Joint Genome Institute.
TITLE Sequencing of Mouse

JOURNAL Unpublished
REFERENCE 2 (bases 1 to 185839)
AUTHORS DOE Joint Genome Institute.
TITLE Direct Submission
JOURNAL Submitted (02-SEP-2000) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
COMMENT -----Genome Center
Center: Joint Genome Institute
Center Code: JGI
Web site: <http://www.jgi.doe.gov>

Project Information
Center Project Name: 1909420
Center clone name: RPCI-23_449F12

Summary Statistics
Consensus quality: 172503 bases at least Q40
Consensus quality: 177768 bases at least Q20
Consensus quality: 179073 bases at least Q20
Estimated insert size: 187000; agarose-fp estimation
Estimated insert size: 184339; sum-of-ctrls estimation
Quality coverage: 7.81 in Q20 bases; agarose-fp estimation
Quality coverage: 7.93 in Q20 bases; sum-of-ctrls estimation.
NOTE: This is a 'working draft' sequence. It currently
* consists of 16 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

1 1081: contig of 1081 bp in length
* 1082 1181: gap of unknown length
* 1182 4298: contig of 3117 bp in length
* 4299 4398: gap of unknown length
* 4399 6733: contig of 2334 bp in length
* 6733 6832: gap of unknown length
* 6832 11626: contig of 4794 bp in length
* 11627 11726: gap of unknown length
* 11727 15445: contig of 3819 bp in length
* 15446 15645: gap of unknown length
* 15646 20007: contig of 4362 bp in length
* 20008 20107: gap of unknown length
* 20108 26156: contig of 6049 bp in length
* 26157 26256: gap of unknown length
* 26257 32958: contig of 6702 bp in length
* 32959 33058: gap of unknown length
* 33059 42014: contig of 8956 bp in length
* 42015 42114: gap of unknown length
* 42115 50688: contig of 8574 bp in length
* 50689 61298: contig of 10510 bp in length
* 61299 61398: gap of unknown length
* 61399 77269: contig of 15871 bp in length
* 77270 77370 77369: gap of unknown length
* 77370 95693: contig of 18324 bp in length
* 95694 95793: gap of unknown length
* 95794 119999: contig of 24206 bp in length
* 120000 120099: gap of unknown length
* 120100 150273: contig of 30174 bp in length
* 150274 150373: gap of unknown length
* 150374 185839: contig of 35466 bp in length.

FEATURES
source 1. 185839
Location/Qualifiers
/organism="Mus musculus"
/db_xref="taxon:10090"
/clone="RP23-449F12"

BASE COUNT 48719 a 43498 c 42466 g 49655 t 1501 others
ORIGIN

Query Match 90.4%; Score 592.8; DB 2; Length 185839;
Best Local Similarity 93.3%; Pred. No. 2.7e-127;

Matches 625; Conservative 0; Mismatches 29; Indels 2; Gaps 2;

OY 1 TATGGCTTCACTGTGACCTTGCCTCTGACGCCACCTGCTGCTGCCCGGCCCTC 60
Db 57586 TATGGCTTCACTGTGACCTTGCCTCTGACGCCACCTGCTGCTGCCCGGCCCTC 57528
OY 61 TGGCCCTTGAAGGCCGCCAGCTTGTGCTGTATGCCCGGCCCGGCCAGG 120
Db 57527 TGGCCCTTGAAGGCCGCCAGCTTGTGCTGTATGCCCGGCCCGGCCAGG 57468
OY 121 CCGGCTTCCGCTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 180
Db 57467 CCGGCTTCCGCTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 57408
OY 181 AGTCATTGAACCGCTGATGAAGAGAGGGGTTTGTGTGTGAAAAAGGCGCTTACGATC 240
Db 57407 AGTCATTGAACCGCTGATGAAGAGAGGGGTTTGTGTGTGAAAAAGGCGCTTACGATC 57348
OY 241 TACTGACCAACCATCGGGCGCTTGGCGGCTTTGGCGCTCATACCATCGGCATCAGACTG 300
Db 57347 TACTGACCAACCATCGGGCGCTTGGCGGCTTTGGCGCTCATACCATCGGCATCAGACTG 57288
OY 301 ACTAGTGGCTTACACAAAGAGCTCTATCTGCAACACCAACCTCAGCAGGATGAT 360
Db 57287 ACTAGTGGCTTACACAAAGAGCTCTATCTGCAACACCAACCTCAGCAGGATGAT 57228
OY 361 ACGGACCAACCCATCGTGGGGGCACTGCTCTCCGAGAGAGAGACCCCTGGGCTTCA 420
Db 57227 ACGGACCAACCCATCGTGGGGGCACTGCTCTCCGAGAGAGAGACCCCTGGGCTTCA 57168
OY 421 CACATTCAAGGCTTGGCGGATATGCTGCTGCGGAGAGATAGGCTGACAGAGGCCCTGGCT 480
Db 57167 CACATTCAAGGCTTGGCGGATATGCTGCTGCGGAGAGATAGGCTGACAGAGGCCCTGGCT 57108
OY 481 GGGCAGCTCCGCTGAGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 540
Db 57107 GGGCAGCTCCGCTGAGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 57048
OY 541 CCCAAGGCTTGAAGGGGTGTGCTTACTGCTGAGAGGCGGATTCATGACACCCCTTCA 600
Db 57047 CCCAAGGCTTGAAGGGGTGTGCTTACTGCTGAGAGGCGGATTCATGACACCCCTTCA 56988
OY 601 TNCCTNTTACAAATCCCTCTTGGGATTTTNGTGTATTTTATTTTCTTTG 656
Db 56987 TNCCTNTTACAAATCCCTCTTGGGATTTTNGTGTATTTTATTTTATTTCTTTG 56933

RESULT 2 AC114434/c 178910 bp DNA linear HFG 13-JUL-2002

LOCUS AC114434 178910 bp DNA linear HFG 13-JUL-2002
DEFINITION Rattus norvegicus clone CH230-210C18, *** SEQUENCING IN PROGRESS
***, 60 unordered pieces.

ACCESSION AC114434
VERSION AC114434.2 GI:21737492
KEYWORDS HFG; HFGS; PHASE1.
SOURCE HFGS, PHASE1.
ORGANISM Norway rat.
Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.

REFERENCE 1 (bases 1 to 178910)
Muzny,D.M., Adams,C., Adlo-Oduola,B., All-osman,F.R., Allen,C.,
Alsbrooks,S.L., Amaralunge,H.C., Are,J.R., Ayele,M., Banks,T.,
Barbarta,J., Benton,J., Blinag,K., Blankenburg,K., Bonnin,D.,
Bouch,J., Bowls,S., Brileva,M., Brown,E., Brown,M., Bryant,N.P.,
Buhay,C., Burch,P., Burkett,C., Burrell,K.L., Byrd,N.C.,
Carroll,T.F., Carter,M., Cavazos,S.R., Chacko,D., Chavez,D.,
Chen,G., Chen,R., Chen,Z., Chowdhury,I., Christopoulos,C.,
Cleveland,C.D., Cox,C., Coyle,M.D., Dathorne,S.R., David,R.,
Devila,M.L., Davis,C., Davy-Carroll,L., Dederich,D.A.,
Delaney,K.R., Delgado,O., Denn,A.L., Ding,Y., Dinl,H.H.,
Douthwaite,K.J., Draper,H., Dugan-Rocha,S., Durbin,K.J.,
Earnhart,C., Edgar,D., Edwards,C.C., Elina,J.C., Escotto,M.,

Falls, T., Ferraguto, D., Flagg, N., Ford, J., Foster, P., Frantz, P.,
Gabriel, A., Gao, J., Garcia, A., Garner, T., Garza, N., Gill, R.,
Gorrell, J. H., Cueva, M., Gunaratne, P., Hale, S., Hamilton, K.,
Harris, C., Harris, K., Hart, M., Havlak, P., Hawes, A., Hernandez, J.,
Hernandez, O., Hodgson, A., Hughes, M., Holloway, C., Hollins, B.,
Horn, F., Howard, S., Huber, J., Hult, S., Hume, J., Jackson, L. E.,
Jacobson, B., Jia, Y., Johnson, R., Jolivet, S., Joudah, S.,
Karlsone, E., Kelly, S., Khan, U., King, L., Korvah, J., Kovar, C.,
Krtovic, J., Kuresh, A., Landry, N., Leal, B., Lewis, L. C., Lewis, L.,
Li, J., Li, Z., Lichtarge, O., Lieu, C., Liu, J., Liu, W., Louised, H.,
Lozano, R. J., Lu, X., Lucier, A., Lucier, R., Luna, R., Ma, J.,
Maheshwari, M., Mapua, P., Martin, R., Martindale, A., McGee, E.,
Massey, E., Mawhney, E., McLeod, M. P., Meador, M., Mei, G., Metzger, M.,
Miner, G., Miner, Z., Mitchell, T., Mohabbat, K., Morgan, M., Morris, S.,
Mosier, M., Neal, D., Newton, J., Newton, N., Nguyen, A., Nguyen, N.,
Nguyen, N., Nickerson, E., Nwokenkwo, S., Ogun, M., Okunolu, G.,
Ogunye, N., Oviedo, R., Pace, A., Payton, B., Peary, J., Perez, L.,
Peters, L., Pickens, R., Primus, E., Pu, L. L., Qulles, M., Ren, Y.,
Rivers, M., Rojas, A., Rojibokan, I., Rolfe, M., Ruiz, S., Savary, G.,
Scherer, S., Scott, G., Shen, H., Shostakov, N., Sisson, I.,
Sodergren, E., Sonalke, T., Sparks, A., Stanley, H., Stone, H.,
Sulton, A., Swalek, A., Tabor, P., Tamerisa, A., Tamerisa, K., Tang, H.,
Tansey, J., Taylor, C., Taylor, T., Telford, B., Thomas, N., Thomas, S.,
Usmani, K., Vasquez, L., Vera, V., Villalón, D., Vinson, R., Wang, O.,
Wang, S., Ward-Moore, S., Warren, R., Washington, C., Watlington, S.,
Williams, G., Williamson, A., Wleczek, R., Wooden, S., Worley, K.,
Wu, C., Wu, Y., Wu, Y. F., Zhou, J., Zortilla, S., Nelson, D.,
Weinstock, G., and Gibbs, R.

Unpublished
2 (bases 1 to 178910)

Worley, K. C.
Direct Submission
Submitted (09-MAR-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 178910)

Worley, K. C.
Direct Submission
Submitted (13-JUL-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
On Jul 12, 2002 this sequence version replaced gi:193101225.

----- Genome Center -----
Center: Baylor College of Medicine
Center code: BCM
Web site: <http://www.hgsc.bcm.tmc.edu/>
Contact: hgsc-help@bcm.tmc.edu
----- Project Information -----
Center project name: GPFX
Center clone name: CH230-210C18
----- Summary Statistics -----
Sequencing vector: Plasmid;
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 126357 bases at least Q40
Consensus quality: 130838 bases at least Q30
Consensus quality: 134610 bases at least Q20

----- NOTE: Estimated insert size may differ from sequence length
(see http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html).
* NOTE: This is a 'working draft' sequence. It currently
* consists of 60 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

1 1046: contig of 1046 bp in length
* 1047 1146: gap of unknown length
* 1147 2255: contig of 1109 bp in length
* 2256 2355: gap of unknown length

2356 3425: contig of 1070 bp in length
* 3426 3526: gap of unknown length
* 3527 3526: contig of 1421 bp in length
* 3527 3526: gap of unknown length
* 3527 3526: contig of 1130 bp in length
* 3527 3526: gap of unknown length
* 3527 3526: contig of 1125 bp in length
* 3527 3526: gap of unknown length
* 3527 3526: contig of 1502 bp in length
* 3527 3526: gap of unknown length
* 3527 3526: contig of 1474 bp in length
* 3527 3526: gap of unknown length
* 3527 3526: contig of 1301 bp in length
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* 3527 3526: contig of 1251 bp in length
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* 3527 3526: contig of 1833 bp in length
* 3527 3526: gap of unknown length
* 3527 3526: contig of 2420 bp in length
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* 3527 3526: gap of unknown length
* 3527 3526: contig of 1114 bp in length
* 3527 3526: gap of unknown length
* 3527 3526: contig of 1875 bp in length
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* 3527 3526: contig of 1426 bp in length
* 3527 3526: gap of unknown length
* 3527 3526: contig of 2153 bp in length
* 3527 3526: gap of unknown length
* 3527 3526: contig of 2233 bp in length
* 3527 3526: gap of unknown length
* 3527 3526: contig of 2067 bp in length
* 3527 3526: gap of unknown length
* 3527 3526: contig of 2159 bp in length
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* 3527 3526: gap of unknown length
* 3527 3526: contig of 1835 bp in length
* 3527 3526: gap of unknown length
* 3527 3526: contig of 1696 bp in length
* 3527 3526: gap of unknown length
* 3527 3526: contig of 2608 bp in length
* 3527 3526: gap of unknown length
* 3527 3526: contig of 1748 bp in length
* 3527 3526: gap of unknown length
* 3527 3526: contig of 1737 bp in length
* 3527 3526: gap of unknown length
* 3527 3526: contig of 2231 bp in length
* 3527 3526: gap of unknown length
* 3527 3526: contig of 2742 bp in length
* 3527 3526: gap of unknown length
* 3527 3526: contig of 2336 bp in length

*	67491	gap of unknown length
*	67591	67590: gap of 2948 bp in length
*	70539	70638: gap of unknown length
*	70639	72942: gap of 2304 bp in length
*	72943	73042: gap of unknown length
*	73043	76294: contig of 3252 bp in length
*	76295	76394: gap of unknown length
*	76395	79037: contig of 2643 bp in length
*	79038	79137: gap of unknown length
*	79138	82946: gap of 3809 bp in length
*	82947	83046: gap of unknown length
*	83047	85707: contig of 2661 bp in length
*	85708	85807: gap of unknown length
*	85808	87648: contig of 1841 bp in length
*	87649	87748: gap of unknown length
*	87749	91762: contig of 4014 bp in length
*	91763	91862: gap of unknown length
*	91863	95721: contig of 3859 bp in length
*	95722	95821: gap of unknown length
*	95822	99306: contig of 3485 bp in length
*	99307	99406: gap of unknown length
*	99407	103926: contig of 4520 bp in length
*	103927	104026: gap of unknown length
*	104027	109477: gap of 5451 bp in length
*	109478	109577: gap of unknown length
*	109578	114409: contig of 4832 bp in length
*	114410	114509: gap of unknown length
*	114510	119171: contig of 4662 bp in length
*	119172	119271: gap of unknown length
*	119272	126347: contig of 7076 bp in length

Query Match	80.0%;	Score 525;	DB 2;	Length 178910;
Best Local Similarity	93.5%;	Pred. No. 1.5e-11;		
Matches 565;	Conservative	0;	Mismatches 37;	Indels 2;
				Gaps 2

OY	2	ATGGCTTACACTCTGACCTTGTGCGCTTGACAGCACACGTGTCGGTGGCCCCGGGCCCCCTCT	61
OY	12		
Db	160533	ATGACTTCACACTCTG - ACTTCGGCTCTTGACAGCCACCTGCTCGCTGCCCTTCCCTCTG	160475
OY	62	GGCCCCCTTGAGGCCCCCAGCTTCTGTGCTGTGTGTATCCCCCCAGCCGGCGGACGGC	121
Db	160474	GGCCCCCTTGAGGCCCCCAGCTTCTGTGCTGTGTATCCCCCCAGCCGGCGGACGGC	160415
OY	122	CCGCGCTCCGGTGTGCCCCGGGTGTGGCCACAGGCCCCCGGGTTCGCATGGGTGAACTGGA	181
Db	160414	CCGCGCTCCGGTGTGCCCCGGGTGTGGCCACAGGCCCCCGGGTTCGCATGGGTGAACTGGA	160355
OY	182	GTCATTGAAACGCTGGAATGAGAGAGAGGGTTTTGTGTGTGAAAGGGCCTTCAGGTACT	241
Db	160354	ATCATTTGAAACGCTGGAATGAGAGAGAGGGTTTTGTGTGTGAAAGGGCCTTCAGGTACT	160295
OY	242	ACTATACCACCATGTGGGGCCTTTCGGGGCTTTTGGCTTATATGACATGCGCTACAGCACTGA	301
Db	160294	ACTATACCACCATGTGGGGCCTTTCGGGGCTTTTGGCTTATATGACATGCGCTACAGCACTGA	160235
OY	302	CTACTGGCTCTACACAGAGCTCTCATCTGTCAACACCACCAACCTCACAGAGTGTATGA	361
Db	160234	CTACTGGCTCTACACAGAGCTCTCATCTGTCAACACCACCAACCTCACAGAGTGTATGA	160175
OY	362	CGGACCAACCCCATCTGTGGGGGCACTGGCTCTCTCCGAGAGAGAGACCTTGGGGCCTCAC	421
Db	160174	TGGACCAACCCCATCTGTGGGGGCACTGGCTCTCTCCGAGAGAGAGACCTTGGGGCCTCAC	160115
OY	422	ACATTGAGGCTCTGGGGGGAATATCTGCTCCGTGGAGGTATGGGTGCAGGAAGGCCCTGGCTG	481
Db	160114	ACATTGAGGCTCTGGGGGGAATATCTGCTCCGTGGAGGTATGGGTGCAGGAAGGCCCTGGCTG	160055
OY	482	GGCACTCTCCGTTGTAAGCTGTGCTCCGTCGAGCAAAATCGATCTTATAGTGTTCAGATCTCAAC	541
Db	160054	GGCACTCTCCGTTGTAAGCTGTGCTCCGTCGAGCAAAACGATCTCTATGTTCATATCTTCATC	159955
OY	542	CCAAGNCTTGAGGGGTGTGCTTTACTGTGTGAGGCG - GNTTNAATTCATGACACCCCTCCA	600

Db 159934 CCAAGGCTTGAAGGGGTGTGCTTCACCTGCTGAGAGACATGATTCATTCGATCCCTCTG 159935

QY 601 TNGC 604
|||

Db 159934 TCCC 159931

RESULT 3	AF361350	1380 bp	mRNA	linear	ROD 21-DEC-2001
LOCUS					
DEFINITION	Mus musculus voltage-dependent calcium channel gamma-8 subunit				
ACCESSION	(Cacng8) mRNA, complete cds.				
VERSION	AF361350				
KEYWORDS	AF361350.1 GI:17974533				
SOURCE	Mus musculus.				
ORGANISM	Mus musculus.				

REFERENCE 1 (bases 1 to 1380)
AUTHORS Chu, P.-J., Robertson, H. M., and Best, P. M.
TITLE Calcium channel gamma subunits provide insights into the evolution
of this gene family
JOURNAL Gene 280 (1-2), 37-48 (2001)
MEDLINE 21601102
PMID 11736816
REFERENCE 2 (bases 1 to 1380)
AUTHORS Chu, P.-J., Robertson, H. and Best, P. M.
TITLE Direct Submission
JOURNAL Submitted (14-MAR-2001) Department of Molecular and Integrative

FEATURES	Location/Qualifiers
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/strain="BALB/c"
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GLVLNVIYIERKIPKAGSCGSRSDLLKAGGACGSGGSPALLRLSPYFRIRRSRSRS
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Query Match	59.1%	Score 387.4	DB 10	Length 1380
Best Local Similarity	99.7%	Pred. No. 1.3e-79		
Matches 388, Conservative	0	Mismatches 1	Indels 0	Gaps 0

Qy	69	TGAGGCCCCCAGCTTTCGCTGAGCTGTATCCCCACGCGCGGCACAGGCGCCGCT	128
Db	1	TGAGGCCCCCAGCTTTCGCTGCTGTATCCCCACGCGCGGCACAGGCGCCGCT	60
Qy	129	CCGCTGCCCGGCTGCTGGTACCACGGCCCCCGGTTGGCAGTGTGAAACTGAGATCATTTG	188
Db	61	CCGGTCCCCCGGCTGCTGGTACCACGGCCCCCGGTTGGCAGTGTGAAACTGAGATCATTTG	120
Qy	189	AAACGCTGTGAATGAAGAGAGGGGCTTTGTGCTGTGAAAAAGGCGTTCAAGTACTACTGACC	248
Db	121	AAACGCTGTGAATGAAGAGAGGGGCTTTGTGCTGTGAAAAAGGCGTTCAAGTACTACTGACC	190


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Oy 249 ACCATCGGCGCTTCGGCGCTTTTGGCCCTCATGACATCGCATCGACTGACTG 308
Db 181 ACATCGGCGCGCTTCCTGCGCTTTTGGCTTCATGACATCGCATCGACTGACTG 240
Oy 309 CTCTACACAGAGCTCTGATCTGCAACACACAACTCTACAGAGTGTATGACGACCA 368
Db 241 CTCTACACAGAGCTCTGATCTGCAACACACAACTCTACAGAGTGTATGACGACCA 300
Oy 369 CCCCATCTCTGGGGGCGAGTGGCTCTCCGAGAGAAGACCTGGGGGCTCTACACATTTCA 428
Db 301 CCCCATCTCTGGGGGCGAGTGGCTCTCCGAGAGAAGACCTGGGGGCTCTACACATTTCA 360
Oy 429 GGCCTCTGGCGGATATGCTGCTGGAGAG 457
Db 361 GGCCTCTGGCGGATATGCTGCTGGAGAG 389

RESULT 4
AC128446/c
LOCUS
DEFINITION Rattus norvegicus clone CH230-95B19, *** SEQUENCING IN PROGRESS
AC128446 142388 bp DNA linear HTG 19-JUL-2002
***, 67 unordered pieces.
AC128446
VERSION AC128446.1 GI:21909138
KEYWORDS HTG: HTGS, PHASE1.
SOURCE Rattus norvegicus.
ORGANISM Rattus norvegicus.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
REFERENCE
1 (bases 1 to 142388)
Muzny,D.M., Adams,C., Adlo-Oguzola,B., All-oman,F.R., Allen,C.,
Alshrooke,S.L., Amaratunga,H.C., Are,J.R., Ayale,M., Banks,T.,
Barbata,J., Benton,J., Bimaga,K., Blankenburg,K., Bonnin,D.,
Boruck,J., Bowie,S., Brileva,M., Brown,E., Brown,M., Bryant,N.P.,
Buhay,C., Burch,P., Burkelt,C., Burrell,K.L., Byrd,N.C.,
Carroll,T.F., Carter,M., Cavazos,S.R., Chacko,J., Chavez,D.,
Chen,G., Chen,R., Chen,Z., Chowdhry,I., Christopoulos,C.,
Cleveland,C.D., Cox,C., Coyle,M.D., Dathorne,S.R., David,R.,
Davila,M.L., Davis,C., Davy-Carroll,L., Dederich,D.A.,
DeJany,R.R., Delgado,O., Denn,A.L., Ding,Y., Dinh,H.H.,
Douthwaite,K.J., Draper,H., Dugan-Rocha,S., Durbin,K.J.,
Earnhart,C., Edgar,D., Edwards,C.C., Elhaj,C., Escotto,M.,
Falls,T., Ferraguto,D., Flagg,N., Ford,J., Foster,P., Frantz,P.,
Gabisi,A., Geo,J., Garcia,A., Garner,T., Garza,N., Gill,R.,
Gorell,J.H., Guevara,W., Gunaratne,P., Hale,S., Hamilton,K.,
Harris,C., Harris,K., Hart,M., Havlak,P., Hawes,A., Hernandez,J.,
Hernandez,O., Hodgson,A., Hogues,M., Holloway,C., Hollins,B.,
Hornal,F., Howard,S., Huber,J., Huliy,S., Hume,J., Jackson,L.E.,
Jacobson,B., Jia,Y., Johnson,R., Jolivet,S., Joudah,S.,
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L.J., Li,Z., Licharge,O., Lieu,C., Liu,J., Liu,W., Louised,H.,
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Masse,E., Mawhney,E., McLeod,M.P., Meador,M., Mei,G., Metzger,M.,
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Scherrer,S., Scott,G., Shen,H., Shooshari,N., Sisson,I.,
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Sulton,A., Svatek,A., Tabor,P., Tamerisa,A., Tamerisa,K., Tang,H.,
Tansey,J., Taylor,C., Taylor,T., Telford,B., Thomas,N., Thomas,S.,
Umanai,K., Vasquez,L., Vera,V., Villalob,D., Vinson,R., Wang,O.,
Wang,S., Ward-Moore,S., Warren,R., Washington,C., Wellington,S.,
Williams,G., Williamson,A., Wleceyk,R., Wooden,S., Worley,K.,
Wu,C., Wu,Y., Wu,Y.F., Zhou,J., Zorilla,S., Nelson,D.,
Weinstock,G. and Gibbs,R.
TITLE
JOURNAL
Direct Submission
Unpublished

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REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
2 (bases 1 to 142388)
Mortley,K.C.
Direct Submission
Submitted (19-JUL-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
----- Genome Center
Center: Baylor College of Medicine
Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
----- Project Information
Center project name: GWS
Center clone name: CH230-95B19
----- Summary Statistics
Sequencing vector: Plasmid;
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 77782 bases at least Q40
Consensus quality: 85255 bases at least Q30
Consensus quality: 89224 bases at least Q20
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* NOTE: Estimated insert size may differ from sequence length
* (see http://www.hgsc.bcm.tmc.edu/docs/genbank-draft-data.html).
* NOTE: This is a 'working draft' sequence. It currently
* consists of 67 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
1
1021: contig of 1021 bp in length
1022 1121: gap of unknown length
1122 1297: contig of 1176 bp in length
1298 2397: gap of unknown length
2398 3813: contig of 1416 bp in length
3814 3913: gap of unknown length
3914 5197: contig of 1284 bp in length
5198 5297: gap of unknown length
5298 6341: contig of 1044 bp in length
6342 7746: contig of 1305 bp in length
7747 7847: gap of unknown length
7848 9653: contig of 1807 bp in length
9654 9753: gap of unknown length
9754 11431: contig of 1678 bp in length
11432 11531: gap of unknown length
11532 12796: contig of 1265 bp in length
12797 12896: gap of unknown length
12897 14059: contig of 1163 bp in length
14060 14159: gap of unknown length
14160 15277: contig of 1118 bp in length
15278 15377: gap of unknown length
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16424 16523: gap of unknown length
16524 18113: contig of 1592 bp in length
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18216 19345: contig of 1130 bp in length
19346 19445: gap of unknown length
19446 21241: contig of 1796 bp in length
21242 21341: gap of unknown length
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22597 23853: contig of 1257 bp in length
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Query Match	55.1%;	Score 361.6;	DB 2;	Length 142388;
Best Local Similarity	87.3%;	Pred. No. 1.4e-73;		
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34753	36601: contig of 1849 bp in length			
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36702	38125: contig of 1424 bp in length			
38126	38225: gap of unknown length			
38226	39774: contig of 1549 bp in length			
39775	39874: gap of unknown length			
39875	41054: contig of 1180 bp in length			
41055	42833: contig of 1679 bp in length			
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42834	44167: contig of 1234 bp in length			
42934	44267: gap of unknown length			
44168	45446: contig of 1179 bp in length			
44268	45546: gap of unknown length			
45447	47410: contig of 1864 bp in length			
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62265	62364: gap of unknown length			
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66674	68876: contig of 2203 bp in length			
68877	68976: gap of unknown length			
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70800	72518: contig of 1719 bp in length			
72519	72618: gap of unknown length			
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76689	76788: gap of unknown length			
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80748	83375: contig of 2628 bp in length			
83376	83475: gap of unknown length			
83476	85478: contig of 2003 bp in length			
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90781	93866: contig of 3086 bp in length			
93867	93966: gap of unknown length			
93967	96843: contig of 2877 bp in length			
96844	96943: gap of unknown length			
96944	100706: contig of 3763 bp in length			
100707	100806: gap of unknown length			
100807	103819: contig of 3013 bp in length			
103820	103919: gap of unknown length			
Query Match	55.1%;	Score 361.6;	DB 2;	Length 142388;
Best Local Similarity	87.3%;	Pred. No. 1.4e-73;		

Draft Sequence Produced by DOE Joint Genome Institute
www.jgi.doe.gov
Finishing Completed at Stanford Human Genome Center
www.shgc.stanford.edu
Quality: Phrap Quality >=40 99.9% of Sequence;
Estimated Total Number of Errors is 0.3.
STS Content:
WI-17997 G23480

NOTE: 90954 Ambiguous base. Probably T.

Location/Qualifiers

FEATURES

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BASE COUNT 39393 a 42877 c 44983 g 42744 t

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Best Local Similarity 81.2%; Pred. No. 9e-59; Mismatches 82; Indels 7; Gaps 3;

Matches 384; Conservative 0;

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Db 107335 CTCTGACCCCTCCCGGCGGAGCTCTCTCGCGGCCGCCGCCGCCGCCGCCGCCG 107394

Oy 68 TTGAAGCCCCCACTTCTGCTGCTGTGTAT---CCCCCAAGCCCGGAGCGCC 124

Db 107395 CCCCCGGGCCCCCGCTTCTGCTGCTGTGTATACCCGCCGCCGCCGCCGCCGCCGCC 107454

Oy 125 GCGCTGCGCCCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 184

Db 107455 GCGCCCGCTGCGCCCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 107514

Oy 185 ATTGAACGCTGGAATGAGAAGAGGGGTTGTGTGTGTAAGAGGCGTTCACTACTACT 244

Db 107515 GCTGAAGCGCTGGAACGAAGACGGGCGCTGTGTGCGAAGAGGGGCTGCACTGCTGCT 107574

Oy 245 GACCAACATCGGCGCTTCTGCGGCTTTTGGCTCATGACATCGGCATCAGACATGACTA 304

Db 107575 GACGACGGTGGCGGCTTCTGCGGCTTCTGCGGCTTCTGCGGCTTCTGCGGCTTCTG 107634

Oy 305 CTGCTCTACACAGAGCTTCATCTGCAACACACCAACCTCACAGC---AGTGATGA 361

Db 107635 CTGCTCTACACAGCGCGGCTTCATCTGCAACACACCAACCTCACAGCGCGGCGG 107694

Oy 362 CGGACCAACCCATCTGCGGCGGAGTGCTCTCGGAGAAAGAGACCTGCGGCGCTGAC 421

Db 107695 CGGACCCCAACCGCGGCGGCGGCGGCGCTCGGAGAAAGAGACCCGCGGCGCTGAC 107754

Oy 422 ACATTGACGCTCTGCGGAGATATGCTGCTGGAAGTGGTGCAGAGAGCC 474

Db 107755 GCACGCGGCGCTTGTGAGATCTGCTGCTGGAAGTGGTGCAGAGAGCC 107807

RESULT 6
AP361346 1266 bp mRNA linear ROD 21-DEC-2001

LOCUS AP361346 Rattus norvegicus voltage-dependent calcium channel gamma-8 subunit
DEFINITION (Cacng8) mRNA, complete cds.
ACCESSION AF361346
VERSION AF361346.1 GI:17974525
KEYWORDS Rattus norvegicus.
SOURCE Rattus norvegicus.
ORGANISM Rattus norvegicus.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;

REFERENCE 1 (bases 1 to 1266)
AUTHORS Chu, P.-J., Robertson, H. M. and Best, P. M.
TITLE Calcium channel gamma subunits provide insights into the evolution
of this gene family
JOURNAL Gene 280 (1-2), 37-48 (2001)

MEDLINE 21601102
PUBMED 11738816
REFERENCE 2 (bases 1 to 1266)
AUTHORS Chu, P.-J., Robertson, H. and Best, P. M.
TITLE Direct Submission
JOURNAL Submitted (14-MAR-2001) Department of Molecular and Integrative
Physiology, University of Illinois, 407 S. Goodwin Ave., Urbana, IL
61801, USA

Location/Qualifiers

FEATURES

source

1. 1266
/organism="Rattus norvegicus"
/strain="Sprague-Dawley"
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subunit"

CDS

BASE COUNT 231 a 423 c 413 g 199 t

Query Match 41.1%; Score 269.8; DB 10; Length 1266;

Best Local Similarity 97.5%; Pred. No. 2.7e-52; Mismatches 274; Conservative 0; Indels 0; Gaps 0;

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Db 1 CTGGAGTCAATTAACCGCTGGAATGAAGAGAGGGTTGTGTGTAAGAGGCGTTGAG 60

Oy 237 GTACTACTGACCAACCATCGGCGCTTCTGCGGCTTTTGGCTCATGACATCGCATCAGC 296

Db 61 GTACTACTGACCAACCATCGGCGCTTCTGCGGCTTTTGGCTCATGACATCGCATCAGC 120

Oy 297 ACTGACTACTGCTTACACAAGAGCTTCATCTGCAACACCAACCTCACAGAGGT 356

Db 121 ACTGACTACTGCTTACACAAGAGCTTCATCTGCAACACCAACCTCACAGAGGT 180

Oy 357 GATGACGACCAACCCATCTGTTGGGCGAGTGGCTCTCCGAGAAAGAGACCTGGGGG 416

Db 181 GATGATGACCAACCCATCTGTTGGGCGAGTGGCTCTCCGAGAAAGAGACCTGGGGG 240

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Db 241 CTCACACATTCAGGCTCTGCGGATATGCTCCTGGAAGG 281

RESULT 7
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LOCUS AC022318 Homo sapiens chromosome 19 clone RP11-158G19, WORKING DRAFT
DEFINITION SEQUENCE, 16 unordered pieces.
ACCESSION AC022318
VERSION AC022318.5 GI:15321555
KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE Homo sapiens.
ORGANISM Homo sapiens.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE 1 (bases 1 to 190210)
AUTHORS Waterston, R. H.
TITLE The sequence of Homo sapiens clone

KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
MEDLINE
PUBMED
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
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BASE COUNT
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QY 313 ACACAGAGCTCTATCTGCAACACCAACCTTCACAGCAGGTGATGAGC-----GAC 366
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QY 367 CACCCCATCGTGGGGGAGTGTCTCTCGAAGAGAGAGACCCGCGGGGCTTCACACAT 426
Db 302 CTCACACTCGGGGGGCTGGCGCGCTTCGAGAGAGAGACCCCGCGGCTTCACGACT 361
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Db 362 CGGCGCTCTGGAGAGATCTGCTCGGAAG 392

RESULT 9
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
source
CDS
misc_feature
BASE COUNT
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Query Match
Best Local Similarity
Matches 233; Conservative 0; Mismatches 48; Indels 3; Gaps 1;
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Db 22 CAGGTGCTGTGAAGCGCTGAAGAGAGCGGGCGCTTGTGTGCAAGAGAGGGGTGAG 81
QY 237 GTACTACTGACACCATCGCGGCTTTCGCGCTTTTGGCTTCATGACATGCGCATGAGC 296
Db 82 GTGCTGCTGAGAGAGGTTGGCGCTTTCGCGCTTTCGCGCTTCATGACATGCGCATGAGC 141
QY 297 ACTGACTACTGCTCTACACAAGACTCTCATCTGCAACACACACACCTCAGAGC---A 353
Db 142 ACTGACTACTGCTCTACACAAGCGCGGCTTCATCTGCAACACACACCTCAGAGC 201
QY 354 GGTGTGAGGAGACACACCATCGTGGGGGAGTGGCTTCGCGGAGAGAGAGAGCGG 413
Db 202 GCGGACGAGGAGACACACCATCGCGGGGCGCGGCGCTTGTGAGAGAGAGAGCGG 261
QY 414 GGCCTCAACATTCAGGCTCTGGCGGATATGCTGCTCGGAAG 457
Db 262 GGCTCAACGACCTCGGGGCTTGTGAGAGATCTGCTGCGGAAG 305
RESULT 10
LOCUS
DEFINITION
AF288388 1281 bp mRNA linear PRI 02-JAN-2002
Homo sapiens calcium channel gamma subunit 8 (CACNG8) mRNA, partial cds.

ACCESSION	AF288388	GI:13357179
VERSION	AF288388.1	
KEYWORDS		
SOURCE		
ORGANISM	homo sapiens.	
REFERENCE	homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	
AUTHORS	1 (bases 1 to 1281)	
TITLE	Burgess,D.L., Gefrides,L.A., Foreman,P.J. and Noebels,J.L. A cluster of three novel Ca2+ channel gamma subunit genes on chromosome 19q13.4: evolution and expression profile of the gamma subunit gene family Genomics 71 (3), 339-350 (2001)	
JOURNAL		
MEDLINE	1110751	
PUBMED	21100909	
REFERENCE	2 (bases 1 to 1281)	
AUTHORS	Burgess,D.L., Gefrides,L.A., Foreman,P.J. and Noebels,J.L.	
TITLE	Direct Submission	
JOURNAL	Submitted (20-JUL-2000) Neurology, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA	
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BASE COUNT	183 a 464 c 458 g 176 t	
ORIGIN		
Query Match	26.1%; Score 171; DB 9; Length 1281;	
Best Local Similarity	82.9%; Pred. No. 2.4e-29;	
Matches 208; Conservative	0; Mismatches 40; Indels 3; Gaps 1;	
OY	210 GATTGTGGTGGAAAGAGGGCGTTGAGGATACACACACCATCGGCGCCTTCGGGCT 269	
Db	1 GGCCTCTGTTGGAGAAAGGGGTGCAAGGTGCTGTGACGACGCTGGCGCCTTCGCCGC 60	
OY	270 TTTGGCTCATGACCATGGCCATGACGACATGACTGACTGGCTTACAGACAGACTCTCATC 329	
Db	61 TTGGCCTCATGATGACCATGGCCATGACGACATGACTGACTGACTTACACGGCGCCTCATC 120	
OY	330 TGCACACCAACCAACTCAGAC---AGTGATGACGACACACCCCATGTGGGGGCACT 386	
Db	121 TGCACACCAACCAACTCAGCGCGCGGCGGACGACGGGAGCCCCACACGCGCGGGCGCG 180	
OY	387 GGCCTCTCGAGAAAGAGACCTTGGGGGCTCAACACATTCAGGCGCTCGCGGATATGC 446	
Db	181 GCGCCTCGAGAAAGAGACCCCGCGGCTCAGACGACTCGGGCCTCTGGAGAGATCTCG 240	
OY	447 TGCCTGGAAGG 457	
Db	241 TGCCTGGAAGG 251	
RESULT 11		
LOCUS	AC128446	142388 bp DNA linear HTG 19-JUL-2002

DEFINITION	REFERENCE
Rattus norvegicus clone CH230-95B19, *** SEQUENCING IN PROGRESS	
***, 67 unordered pieces.	
AC128446	
AC128446.1 GI:21909138	
HTG; HTGS_PHASE1.	
Rattus norvegicus	
Rattus norvegicus	
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;	
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;	
Rattus.	
1 (bases 1 to 142388)	
Muzny,D.N., Adams,C., Adio-Oduola,B., Ali-osman,F.R., Allen,C.,	
Aisbrooks,S.L., Amaralunga,H.C., Are,J.R., Ayele,M., Banks,T.,	
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Carroll,T.F., Carter,M., Cavazos,S.R., Chacko,J., Chavez,D.,	
Chen,G., Chen,R., Chen,Z., Chowdhry,I., Christopoulos,C.,	
Cleveland,C.D., Cox,C., Coyle,M.D., Dathorne,S.R., David,R.,	
Dayila,M.L., Davis,C., Davy-Carroll,L., Dederich,D.A.,	
Delaney,K.R., Delgado,O., Denn,A.L., Ding,Y., Dinh,H.H.,	
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Earnheart,C., Edgar,D., Edwards,C.C., Elhaj,S., Escotto,M.,	
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Harris,C., Harris,K., Hart,M., Havlik,P., Hawes,A., Hernandez,J.,	
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Massey,E., Mawhney,E., McLeod,M.P., Meador,M., Mel,G., Metzker,M.,	
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Scheer,S., Scott,G., Shen,H., Shochetari,N., Sisson,I.,	
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Sutton,A., Szatek,A., Tabor,P., Tamerisa,A., Tameris,K., Tang,H.,	
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Usmani,K., Vasquez,L., Vera,V., Villalon,D., Vinson,R., Wang,Q.,	
Wang,S., Ward-Moore,S., Warren,R., Washington,C., Watlington,S.,	
Williams,G., Williamson,A., Wleczyk,R., Wooden,S., Worley,K.,	
Wu,C., Wu,Y., Wu,Y.F., Zhou,J., Zorrilla,S., Nelson,D.,	
Weinstock,G. and Gibbs,R.	
Direct Submission	
Unpublished	
2 (bases 1 to 142388)	
Worley,K.C.	
Direct Submission	
Submitted (19-JUL-2002) Human Genome Sequencing Center, Department	
of Molecular and Human Genetics, Baylor College of Medicine, One	
Baylor Plaza, Houston, TX 77030, USA	
----- Genome Center	
Center: Baylor College of Medicine	
Center code: BCM	
Web site: http://www.hgsc.bcm.tmc.edu/	
Contact: hgsc-help@bcm.tmc.edu	
----- Project Information	
Center project name: GWIS	
Center clone name: CH230-95B19	
----- Summary Statistics	
Sequencing vector: Plasmid;	
Chemistry: Dye-terminator Big Dye; 100% of reads	
Assembly program: Phrap; version 0.990329	
Consensus quality: 77782 bases at least Q40	
Consensus quality: 85255 bases at least Q30	

Consensus quality: 89224 bases at least Q20

* NOTE: Estimated insert size may differ from sequence length
* (see <http://www.bjsc.bcm.tmc.edu/docs/genbank/draft.data.html>).
* NOTE: This is a 'working draft' sequence. It currently
* consists of 67 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

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* 1022 1121: gap of unknown length
* 1122 2297: contig of 1176 bp in length
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* 3814 3913: gap of unknown length
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* 5198 5297: gap of unknown length
* 5298 6341: contig of 1044 bp in length
* 6342 6441: gap of unknown length
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* 7747 7846: gap of unknown length
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* 12797 12896: gap of unknown length
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* 14160 15277: contig of 1118 bp in length
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Best Local Similarity 93.4%; Pred. No. 2,2e-26;
Matches 198; Conservative 0; Mismatches 11; Indels 3; Gaps 3;

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Db 74013 ATGACTTACCTCTG-ACCTCGGCTCTGCACGACCACTGCTGCTGCCCTT-CCCTCT 74070
QY 62 GGGCCCTTGAGAGCCCGCCAGCTTCTGCTGCTGTATCCCGCCAGCGCGGACAGGC 121
Db 74071 GGGCCCTTGAGAGCCCGCCAGCTTCTGCTGCTGTATCCCGCCAGCGCGGACAGGC 74130
QY 122 CCGGCTTCGCTGCGCCCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 181
Db 74131 CCGGCTTCGCTGCGCCCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 74190
QY 182 GTGATTGAACGCTGGAATGAAGAGAGGGTT 213
Db 74191 ATGA-AGAAACGCTGGAATGAAGAGAGGGTT 74221

RESULT 12
LOCUS AY037891 987 bp mRNA linear VRT 01-APR-2002
DEFINITION Gallus gallus calcium channel gamma 4 subunit (CACNG4) mRNA,
complete cds.
ACCESSION AY037891
VERSION AY037891.1 GI:15418940
KEYWORDS
SOURCE
ORGANISM Gallus gallus.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
REFERENCE
AUTHORS 1 (bases 1 to 987)
TITLE Kious,B.M., Baker,C.V., Bronner-Fraser,M. and Knecht,A.K.
Identification and characterization of a calcium channel gamma
subunit expressed in differentiating neurons and myoblasts
Dev. Biol. 243 (2), 249-259 (2002)
JOURNAL
MEDLINE 21881550
PUBMED 11884034
REFERENCE 2 (bases 1 to 987)
AUTHORS Kious,B.M., Bronner-Fraser,M. and Knecht,A.K.
TITLE Direct Submission
JOURNAL Submitted (04-JUN-2001) Biology, Caltech, Mail Code 139-74,
Pasadena, CA 91125, USA
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Best Local Similarity 65.9%; Pred. No. 5.3e-11;
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OY 274 GCCTCATGACATCGCATCAGACATGACTGCTGCTACACAAGAGCTTCATCTGCA 333
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OY 394 CCGAAGAAGAGACCTGGGGGCTCAGACATTCAGGCGCTTGGGGATATGCTGCTGG 453
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OY 454 AAGGTA 459
AUTHORS
TITLE
JOURNAL
FEATURES
221 AAGGAA 226

RESULT 13
LOCUS HSCACNG1 720 bp DNA linear PRI 07-JAN-2000
DEFINITION Homo sapiens calcium channel gamma 4 subunit (CACNG4) gene, exon 1.
ACCESSION AF142622
VERSION AF142622.1 GI:6062998
KEYWORDS
SEGMENT 1 of 4
SOURCE
ORGANISM Homo sapiens.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
AUTHORS 1 (bases 1 to 720)
TITLE Burgess,D.L., Davis,C.F., Gefridés,L.A. and Noebels,J.L.
Identification of three novel Ca(2+) channel gamma subunit genes
reveals molecular diversification by tandem and chromosome
duplication
Genome Res. 9 (12), 1204-1213 (1999)
JOURNAL
MEDLINE 20082967
PUBMED 10613843
REFERENCE 2 (bases 1 to 720)
AUTHORS Burgess,D.L., Caleb,D.F., Lisa,G.A. and Jeffrey,N.L.
TITLE Direct Submission
JOURNAL Submitted (12-APR-1999) Neurology, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
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Best Local Similarity 66.8%; Pred. No. 1.1e-09;
Matches 123; Conservative 0; Mismatches 61; Indels 0; Gaps 0;
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DB 299 GCCTCATGCGCATTCGCGCATCGGTACCGACTACTGGCTGACTCAGCGGCGCATCTGCA 358
OY 334 ACACCAACACCTCAGACGAGTATGACGACACACCCCATGCTGGGGGAGTGGCTCCT 393
DB 359 ACGGACCAACATCAGACGAGTATGACGAGGCGGCCCGCGCGCGCGGCGGCGACTCA 418
OY 394 CCGA 397
DB 419 CCCA 422
RESULT 14
LOCUS AR165149 984 bp DNA linear PAT 17-OCT-2001
DEFINITION Sequence 1 from patent US 6274380.
ACCESSION AR165149
VERSION AR165149.1 GI:16238585
KEYWORDS
SOURCE
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 984)
AUTHORS Duckworth,D., Malcolm, and Hayes,P. David.
TITLE Ccnglike3 polynucleotides and expression systems
JOURNAL Patent: US 6274380-A 1 14-AUG-2001;
Location/Qualifiers

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: February 9, 2003, 18:41:53 ; Search time 225 Seconds

(without assignments)

6565.826 Million cell updates/sec

Title: US-10-060-066-2

Sequence: 1 tatgcttcactctgcact.....tgattattttatttctcttg 656

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 4370478

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Minimum DB seq length: 0
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Maximum DB seq length: 200000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : N_Geneseq_101002:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	86.4	13.2	984	21	AAZ99791	DNA encoding a vol
2	86.4	13.2	984	22	AAAF81301	Human cdc98 CDNA
3	83.2	12.7	1071	24	ABK51918	cDNA encoding mouse
4	73.2	11.2	1093	24	ABQ17108	Oligonucleotide f
5	73.2	11.2	1093	24	ABQ17108	Oligonucleotide f
6	54.4	8.3	972	21	AAZ99795	DNA encoding a vol
7	54.4	8.3	1252	22	ABA09049	Human voltage gate
8	54.4	8.3	1478	21	AAZ51628	Human membrane cha
9	53.6	8.2	1477	24	ABK51914	cDNA encoding mouse

10	52.8	8.0	1558	24	ABK51913	CD4 encoding mouse
11	52	7.9	945	21	AAZ99794	EST crossponding
12	52	7.9	948	21	AAZ99793	DNA encoding a neu
13	52	7.9	1383	22	ABA09004	Human voltage gate
14	52	7.9	1854	21	BAAC7216	Human ORFX ORF2711
15	42.8	6.5	799	19	AAV55831	Nucleotide sequenc
16	42.8	6.5	1925	20	AAV50924	Epstein Barr Virus
17	42.8	6.5	1926	21	AAAS0254	Epstein Barr virus
18	42.8	6.5	1926	22	AAFE2902	EBV tethering prob
19	42.8	6.5	2580	21	AAAY5454	Nucleotide sequenc
20	42.8	6.5	2580	24	AA164275	Epstein-Barr virus
21	42.8	6.5	5452	20	AAK30923	Anti-sense strand
22	42.8	6.5	8700	20	AAZ23778	Vector psbHt1e DR
23	42.8	6.5	9600	19	AAV21683	Vector psbHt1e DR
24	42.8	6.5	10380	20	AAZ22248	Nucleotide sequenc
25	42.8	6.5	10596	14	AAQ51731	Plasmid pCISEBON f
26	42.8	6.5	10596	17	AAAT40348	Plasmid pCISEBON f
27	42.8	6.5	10596	20	AAK15650	Nucleotide sequenc
28	42.8	6.5	16080	21	AAAS9553	DNA clone pCEK C1
29	42.6	6.5	585	24	ABOS0506	Oligonucleotide fd
30	42.6	6.5	585	24	ABOS0507	Oligonucleotide fd
31	42.4	6.5	1000	21	AAK02484	Human colon cancer
32	41.8	6.4	415	22	AA182119	Human polynucleoti
33	41.6	6.3	541	21	AAIC07568	Human secreted pro
34	41.6	6.3	1646	21	AAZ35959	S. klatsensis m
35	41.4	6.3	114793	22	AAAD08215	Human genome from
36	41.2	6.3	594	24	ABO43958	Oligonucleotide fd
37	41.2	6.3	3300	24	ABO43959	Oligonucleotide fd
38	41.2	6.3	3300	24	AB158767	Human A013 encodin
39	41.2	6.3	8008	20	AAZ32024	Human MTH1 relate
40	41.2	6.3	8009	22	AAAC30081	X95959 CDNA clone
41	41	6.2	1098	23	AA567509	DNA encoding novel
42	40.8	6.2	1127	21	AAA02477	Human colon cancer
43	40.6	6.2	600	24	ABOS2457	Oligonucleotide fd
44	40.6	6.2	600	24	ABO52456	Oligonucleotide fd
45	40.6	6.2	7732	22	ABA20250	Human nervous syst

ALIGNMENTS

RESULT	1
AAZ99791	
ID	AAZ99791 standard; DNA; 984 BP.
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XX	
AC	AAZ99791;
XX	
DT	12-JUL-2000 (first entry)
XX	
DE	DNA encoding a voltage-gated calcium channel designated CACNGLIKE3.
XX	
XX	Human; skeletal muscle; voltage-gated calcium channel; CACNGLIKE3;
KW	neurological disorder; epilepsy; stroke; head trauma; migraine;
KW	affective disorder; depression; anxiety; schizophrenia; pain; cancer
KW	neurodegenerative disorder; Alzheimer's disease; cognitive disorder;
KW	chromosome localisation; ss.
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OS	Homo sapiens.
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FH	Key
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PN	WO200014224-A1.
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PD	16-MAR-2000.
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PF	06-SEP-1999; 99WO-GB02944.
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PR	08-SEP-1998; 98GB-0019592.
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PA	(SMIK) SMITHKLINE BEECHAM PLC.

PI	Duckworth DM, Hayes PD;
XX	
DR	WPI; 2000-256976/72.
XX	
P-PSDB; AAY84372.	
PT	Isolated voltage-gated calcium channel polypeptide, designated
CC	CACNGLIKE3, to treat diseases such as neurological disorders, epilepsy,
PT	neurodegenerative disorders, cognitive disorders and cancer; comprises
PT	327 amino acid sequence -
XX	
PS	Claim 4; Page 31; 37pp; English.
XX	
CC	The present sequence encodes a human skeletal muscle voltage-gated
CC	calcium channel polypeptide, designated CACNGLIKE3. The CACNGLIKE3
CC	polypeptide and polynucleotide are useful in the treatment of diseases
CC	such as neurological disorders, epilepsy, stroke, head trauma, migraine,
CC	affective disorders including depression and anxiety, schizophrenia,
CC	neurodegenerative disorders including Alzheimer's disease, cognitive
CC	disorders, types of pain and cancer. The polynucleotide is also valuable
CC	for chromosome localisation studies. The CACNGLIKE3 polypeptide and
CC	polynucleotide are also useful in diagnostic assays for detecting
CC	diseases associated with inappropriate CACNGLIKE3 activity or levels.
XX	
SO	Sequence 984 BP; 206 A; 319 C; 265 G; 194 T; 0 other:
	Query Match 13.2%; Score 86.4; DB 21; Length 984;
	Best Local Similarity 66.8%; Pred. No. 1e-12;
	Matches 123; Conservative 0; Mismatches 61; Indels 0; Gaps 0;
OY	214 TGTGTTGTAAGAAGCGCTTCAGTACTGATGCACCATCGGCCCTTCGGCCTTTG 273
Db	5 TGCATGCGGACCGCGGCTCGCATGCTGCTGATACCAGCGCCGAGCCTTCCGCGCTTCT 64
OY	274 GCCTTCATGACCATCGCATGCATCAAGCTGCTCTACACAAGAGCTCATCTGCA 333
Db	65 CGCTCATGGCCATCGCATCGGCACGACTACTGGCTGATCCAGCGGACATCTGCA 124
OY	334 ACACCCACCACTCTCACAGCAGTGATGAAGGACACCCCATTGTTGGGGCAGTGGCTCT 393
Db	125 ACGGACCCAACTGACATGAGCAGCGGGCCCCCGCGCGCGCGGCGGACCTCA 184
OY	394 CGCA 397
Db	185 CCCA 188
RESULT 2	
AAP81301	
ID	AAP81301 standard; cDNA; 984 BP.
XX	
AC	AAP81301;
XX	
DT	01-JUN-2001 (first entry)
DE	
XX	Human cacng8 cDNA.
XX	
KM	Human; stargazin-like; CACNG8; anticonvulsant; hypotensive; vasotropic;
KM	antiarrhythmic; antianginal; analgesic; nootropic; cyostatic;
KM	neuroprotective; cerebroprotective; antidepressant; antimigraine;
KM	antiarteriosclerotic; immunosuppressive; antiparkinsonian; auditory;
KM	ophthalmological; tranquiliser; neuronal disorder;
KM	calcium channel modulation; ss.
XX	
OS	Homo sapiens.
XX	
PN	WO200121791-A2.
XX	
PD	29-MAR-2001.
XX	
PE	25-SEP-2000; 2000WO-GB03685.
XX	
PR	23-SEP-1999; 99GB-0022571.

[illegible]

FT		/tag= a
FT	CDS	22..1005
FT		/*tag= b
FT		/product= "Cacng4 #1"
FT	CDS	22..1005
FT		/*tag= c
FT		/product= "Cacng4 #2
FT		/transl_except= (pos:979..981, aa:Xaa)
FT		/transl_except= (pos:991..993, aa:Xaa)
FT		/note= "Xaa= unknown"
FT	3' UTR	1006..1071
FT		/*tag= d
XX		
PN	US6365337-B1.	
PD	02-APR-2002.	
XX		
PE	27-JUL-1998;	980S-0123030.
PR	27-JUL-1998;	980S-0123030.
XX	(IOMA) UNIT IOWA RES FOUND.	
PA	(JACK-) JACKSON LAB.	
XX		
PI	Letts VA, Frankel WN, Campbell KP, Felix R, Biddlecome G;	
DR	WPI: 2002-433421/46.	
XX	P-PSDB; AAU97155, AAU97156.	
PT	Novel nucleic acid sequences encoding a neuronal voltage-gated calcium channel gamma subunit useful in screening for compounds which modulate activity of the channel and in diagnosing, treating neuronal diseases	
PT	-	
XX		
PS	Disclosure: Fig 7; 36pp: English.	
XX		
CC	The present invention relates to the isolation of mouse genes encoding neuronal voltage-gated calcium channel gamma subunits designated Cacng2, Cacng3, and Cacng4. The genes are useful for identifying candidate compounds for modulating the activity of human neuronal voltage-gated calcium channels. They are also useful for diagnosing and treating the autoimmune disease Lambert-Eaton syndrome, as well as diagnosing defects in gamma subunit genes of a patient with a neuronal disease such as epilepsy. The present sequence encodes mouse Cacng4.	
CC	Note: Nucleotides 1-21 of the present sequence are not shown in Fig 7 but are included in the sequence shown in the sequence listing.	
CC		
XX		
SQ	Sequence 1071 BP: 227 A; 345 C; 284 G; 213 T; 2 other:	
	Query Match 12.7%; Score 83.2; DB 24; Length 1071;	
	Best Local Similarity 65.8%; Pred. No. 7.le-12;	
	Matches 121: Conservative 0; Mismatches 63; Indels 0; Gaps 0;	
OY	214 TGTGGTGAAGAAGGCGCTTCAGTACTAGTACCAACCATCGGCGGCTTCGCGGCTTTTG 273	
Db	26 TGCGATGGGACCGGGGCTGCAGATGCTGTCTACCAAGCGCGGAGCCCTTCGCCCTTTCT 85	
OY	274 GCCTCATGACCATTCGCCATTCAGCACACTGAGCTTAGCAGTCTACACAAGAGCTTCATCTGCA 333	
Db	86 CGCTCATGCGCATTCGCCATTCGCGACCGAGCTACCGGCTGTATCTCAAGCCGCGACATCTGCA 145	
OY	334 ACACCAACCAACTCAGCAGCAGGTGATGACGAGCACACCCCATCTGTGGGGGCAAGTGGCTCT 393	
Db	146 ACGGCAACCAACTGACATGACGACGAGGCCCCCGCCCGCGCTTCGCGGAGACTCA 205	
OY	394 CCGA 397	
Db	206 CCCA 209	
RESULT	4	

AB017108/C	AB017108 standard: DNA; 1093 BP.
ID	AB017108
AC	AB017108;
XX	
XX	
DT	12-JUL-2002 (first entry)
XX	
DE	Oligonucleotide for detecting cytosine methylation SEQ ID NO 3699.
XX	
KW	Human; cytosine methylation; 5'-CpG-3'; uracil; cytosine; diagnosis;
KW	drug; side effect; cancer; central nervous system; cardiovascular;
KW	gastrointestinal; respiratory system; single nucleotide polymorphism;
KW	SNP; cell differentiation; ds.
XX	
OS	Homo sapiens.
XX	
PN	WO200218632-A2.
XX	
PD	07-MAR-2002.
XX	
PF	01-SEP-2001; 2001WO-EP10074.
XX	
PR	01-SEP-2000; 2000DE-1043826.
PR	05-SEP-2000; 2000DE-1044543.
XX	
PA	(EPIG-) EPIGENOMICS AG.
PI	Olek A, Piepenbrock C, Berlin K, Guetig D;
XX	
DR	WPI: 2002-371829/40.
XX	
PT	Determining the degree of cytosine methylation in genomic DNA, useful
PT	for diagnosis and prognosis, comprises selective hybridization of
PT	amplicons from chemically treated DNA -
PS	Claim 12; 56pp + Sequence Listing; 56pp; German.
XX	
XX	This invention describes a novel method for determining the degree of
CC	methylation of a particular cytosine in a motif 5'-CpG-3', present in a
CC	genomic sample of DNA. The sample is treated chemically to convert
CC	cytosine (C) but not methylated C, to uracil, then part of the genomic
CC	DNA that contains the target C is amplified to form a labeled amplicon.
CC	The amplicon is hybridised to two classes, each with at least one
CC	member, of oligonucleotides and/or peptide-nucleic acid (PNA) oligomers
CC	and the degree of hybridisation to both classes is determined from the
CC	label on the amplicon. From the ratio of labels hybridised to the two
CC	classes of oligomers, the degree of methylation is calculated. The method
CC	is used: (i) for diagnosis and/or prognosis of side effects of
CC	therapeutic drugs and of a wide range of diseases, e.g. cancer, disorders
CC	of the central nervous, cardiovascular, gastrointestinal and respiratory
CC	systems etc., particularly by detecting mutations or single nucleotide
CC	polymorphisms (SNP's); and (ii) for differentiation of cell or tissue
CC	types and for investigating cell differentiation. The method allows the
CC	methylation status of many C residues to be determined simultaneously.
CC	AB013410-AB054121 represent genomic DNA sequences used to illustrate the
CC	method for determining the degree of cytosine methylation described in
CC	the disclosure of the invention.
XX	
SQ	Sequence 1093 BP; 95 A; 153 C; 406 G; 439 T; 0 other;
XX	
Query Match	11.2%; Score 73.2; DB 24; Length 1093;
Best Local Similarity	65.1%; Pred. No. 2.9e-09;
Matches 108; Conservative	0; Mismatches 58; Indels 0; Gaps 0;
QY	232 TTCAGTACTACTGACACCAATCGGCGCTTGGCGCTTTGGCCATGACCAATCGCA 291
DB	683 TACCAATACTACTAACACGACGACCAAACTTGGCCGCTTCGCTCAATACCAATCGCA 624
QY	292 TCAGACCTACTACTGCGCTACACAAAGAGCTCTCTGCAACACCAACCACTCAG 351
DB	623 TCGACACGACCTACTACTATATCTCCACAGCGGCACATCTCAACAGACCAACCTAACCA 564
QY	352 CAGGTGATGACGAGACCCCATCTGCGGGGAGTGGCTCTTCGCA 397

Db 563 TAAAGCAGAACCCCGCCGCGCGCGAGCAGACTACCA 518

RESULT 5
AB017109
ID AB017109 standard; DNA; 1093 BP.

AC AB017109;

DT 12-JUL-2002 (first entry)

DE Oligonucleotide for detecting cytosine methylation SEQ ID NO 3700.

Human; cytosine methylation; 5'-CpG-3'; uracil; cytosine; diagnosis;
drug; side effect; cancer; central nervous system; cardiovascular;
KW gastrointestinal; respiratory system; single nucleotide polymorphism;
SNP; cell differentiation; ds.

OS Homo sapiens.

PN WO200218632-A2.

PD 07-MAR-2002.

PF 01-SEP-2001; 2001WO-EP10074.

PR 01-SEP-2000; 2000DE-1043826.

PR 05-SEP-2000; 2000DE-1044543.

PA (EPIC-) EPIGENOMICS AG.

PI Olek A, Piepenbrock C, Berlin K, Guetig D;

DR WPI; 2002-371829/40.

PT Determining the degree of cytosine methylation in genomic DNA, useful
for diagnosis and prognosis, comprises selective hybridization of
amplicons from chemically treated DNA -

PS Claim 12; 56pp + Sequence Listing; 56pp; German.

CC This invention describes a novel method for determining the degree of
methylation of a particular cytosine in a motif 5'-CpG-3', present in a
genomic sample of DNA. The sample is treated chemically to convert
cytosine (C) but not methylated C, to uracil, then part of the genomic
DNA that contains the target C is amplified to form a labeled amplicon.
The amplicon is hybridised to two classes, each with at least one
member, of oligonucleotides and/or peptide-nucleic acid (PNA) oligomers
and the degree of hybridisation to both classes is determined from the
label on the amplicon. From the ratio of labels hybridised to the two
classes of oligomers, the degree of methylation is calculated. The method
is used: (i) for diagnosis and/or prognosis of side effects of
therapeutic drugs and of a wide range of diseases, e.g. cancer, disorders
of the central nervous, cardiovascular, gastrointestinal and respiratory
systems etc., particularly by detecting mutations or single nucleotide
polymorphisms (SNP's); and (ii) for differentiation of cell or tissue
types and for investigating cell differentiation. The method allows the
methylation status of many C residues to be determined simultaneously.
AB013410-AB054121 represent genomic DNA sequences used to illustrate the
method for determining the degree of cytosine methylation described in
the disclosure of the invention.

CC Sequence 1093 BP; 439 A; 406 C; 153 G; 95 T; 0 other;

Query Match 11.2%; Score 73.2; DB 24; Length 1093;

Best Local Similarity 65.1%; Pred. No. 2.9e-09;

Matches 108; Conservative 0; Mismatches 58; Indels 0; Gaps 0;

OY 232 TTCAGTACTACGACACCATCGGCGCTTTCGGCTTTGGCCATGACATGCGCA 291

DB 411 TACAAATACTACTACGACGACCAACCTTCCGCCCTTTCGCTCATTAACCATGCGCA 470

OY 292 TCAGCAGTACTACTGCTCTACACAGAGCTCTCATCTGCACACACCACTCAG 351
DB 471 TCGACACCGACTACTACTATCCACGCGCATCTTAACGACACCACTTAACCA 530

OY 352 CAGGTGATGACGACGACCCCATCGTGGGGGAGTGATGCTCTCCGA 397

DB 531 TAAAGCAGAACCCCGCCGCGCGCGAGCAGACTACCA 576

RESULT 6
AA299795
ID AA299795 standard; DNA; 972 BP.

AC AA299795;

DT 12-JUL-2000 (first entry)

DE DNA encoding a voltage-gated calcium channel designated CACNG1IKE1.

Human; voltage-gated calcium channel; CACNG1IKE1; neurological disorder;
epilepsy; stroke; head trauma; migraine; affective disorder; depression;
anxiety; schizophrenia; neurodegenerative disorder; Alzheimer's disease;
cognitive disorder; pain; cancer; chromosome localization; ss.

OS Homo sapiens.

Key Location/Qualifiers

FT CDS 1..972

FT /tag= a

FT /product= "voltage-gated calcium channel"

PN WO200014223-A1.

PD 16-MAR-2000.

PF 06-SEP-1999; 99WO-GB02937.

PR 07-SEP-1998; 98GB-0019474.

PA (SMIK) SMITHKLINE BEECHAM PLC.

PI Duckworth DM, Hayes PD;

DR WPI; 2000-256975/22.

DR P-PSDB; AAY84376.

PT New human voltage-gated calcium channel, known as CACNG1IKE1, useful in
the treatment of diseases such as neurological disorders, epilepsy,
neurodegenerative disorders, cognitive disorders and cancer, comprises
a 323 amino acid sequence -

PS Claim 4; Page 30; 35pp; English.

CC The present sequence encodes a human voltage-gated calcium channel,
known as CACNG1IKE1. The CACNG1IKE1 polypeptide and polynucleotide are
useful in the treatment of diseases such as neurological disorders,
epilepsy, stroke, head trauma, migraine, affective disorders including
depression and anxiety, schizophrenia, neurodegenerative disorders
including Alzheimer's disease, cognitive disorders, types of pain and
cancer. The polynucleotide is also valuable for chromosome localization
studies. CACNG1IKE1 polypeptide and polynucleotide are also useful in
diagnostic assays for detecting diseases associated with inappropriate
CACNG1IKE1 activity or levels.

CC Sequence 972 BP; 231 A; 311 C; 231 G; 199 T; 0 other;

Query Match 8.3%; Score 54.4; DB 21; Length 972;

Best Local Similarity 70.2%; Pred. No. 0.00022;

Matches 73; Conservative 0; Mismatches 31; Indels 0; Gaps 0;

OY 218 GTGTGAAAAGGCGCTTACGACTGACACCATCGGCGCTTGGCGGCTTTGGCCT 277

DB 9 GTTGTGAGGAGTGTCAATGCTTTTAACACACCGTTGGTGTCTTGCCTTCAAGCCT 68

Oy 278 CATGACCATCGCATGACACTGACTGCTACACAGAG 321
 ||||| 11 11 ||||| ||||| 1111
 Db 69 GATGACCATGCTGTGGACCGACTATGTGCTTACTCCAGAG 112

RESULT 7
 ABA09049
 ID ABA09049 standard; cDNA; 1252 BP.
 XX
 AC ABA09049;
 DT 11-JAN-2002 (first entry)
 XX

Human voltage gated Ca channel subunit homologue cDNA, SEQ ID NO:825.
 XX
 XX Human; cytokine; cell proliferation; cell differentiation; growth factor;
 KM haematopoiesis regulation; tissue growth; immunomodulator; activin;
 KM lymphin; chemotaxis; chemokinesis; thrombolysis; oncogenesis;
 KM proliferation; metastasis; cancer; tumour; haematopoietic disorder;
 KM myeloid cell disorder; lymphoid cell disorder; asthma; arthritis;
 KM chronic inflammatory condition; proliferative retinopathy;
 KM atherosclerosis; coronary heart disease; arterial ischaemia;
 KM bone disorder; osteoporosis; vascular growth disorder;
 KM tissue regeneration; wound healing; infection; immune disorder;
 KM cell culture; drug screening; gene therapy; antiinflammatory;
 KM antihistaminic; antiarthritic; haemostatic; antiarteriosclerotic;
 KM cytoskeletal; osteopathic; vasotropic; cardiant; antibacterial;
 KM antifungal; vulninary; antinicer; ss.
 XX
 OS Homo sapiens.
 PN W0200157188-A2.
 PD 09-AUG-2001.
 XX
 PF 05-FEB-2001; 2001WO-US03800.
 PR 03-FEB-2000; 2000US-0496914.
 PR 27-APR-2000; 2000US-0560875.
 XX
 PA (HYSE-) HYSEQ INC.
 PI Tang YT, Liu C, Dymnac RT;
 XX
 DR WPI; 2001-457740/49.
 XX
 PT P-PSDB; ABB11805.
 PT Human proteins and DNA encoding sequences useful for preventing,
 PT treating or ameliorating a medical condition in a mammalian subject
 PT e.g. arthritis and cancer -
 XX
 PS Claim 1; Page 731-732; 1963pp; English.
 CC Sequences ABB10981-ABB12330 represent 1350 novel human polypeptides, and
 CC sequences ABA08225-ABA09574 represent nucleic acids encoding them. The
 CC invention also relates to vectors and recombinant host cells comprising a
 CC nucleotide of the invention, methods of producing the novel polypeptides,
 CC antibodies against the polypeptides, methods of detecting the nucleotides
 CC or polypeptides in a sample, and methods of identifying compounds which
 CC bind to polypeptides of the invention. Although novel, many of the
 CC polypeptides of the invention have homology to known proteins, thereby
 CC giving an insight into their probable biological activities, and hence
 CC potential therapeutic applications. The polypeptides of the invention may
 CC have various activities, including cytokine, cell proliferation or cell
 CC differentiation activities; stem cell growth factor activity;
 CC haematopoiesis regulatory activity; tissue growth activity;
 CC immunomodulatory activity; activin- or inhibin-related activities;
 CC chemotactic or chemokinetic activities; haemostatic, thrombotic or
 CC thrombolytic activities; receptor or ligand activities. Or may be
 CC involved in oncogenesis, cancer cell proliferation or metastasis.
 CC Depending on their biological activities, polypeptides and nucleotides of
 CC the invention are useful for preventing, treating or ameliorating medical

CC conditions, e.g., by protein or gene therapy. Such conditions include
 CC cancers, haematopoietic disorders (e.g., myeloid or lymphoid cell
 CC disorders), chronic inflammatory conditions (e.g., asthma or arthritis),
 CC proliferative retinopathy, atherosclerosis, coronary heart disease,
 CC arterial ischaemia, bone disorders (e.g., osteoporosis), and abnormal
 CC vascular growth. Polypeptides involved in tissue regeneration and
 CC repair (or nucleic acids encoding them) may be used to promote wound
 CC healing (e.g., of burns, incisions and ulcers), while those with
 CC immunomodulatory activities may be used in the treatment of viral,
 CC bacterial and fungal infections in addition to immune disorders.
 CC Polypeptides with growth factor activity may be used in cell cultures to
 CC promote cell growth. For example, such polypeptides may be used to
 CC manipulate stem cells in culture to give rise to neuroepithelial cells
 CC that can be used to augment or replace cells damaged by illness,
 CC autoimmune disease or accidental damage. The polypeptides and nucleotides
 CC may also be used in the diagnosis of the above conditions, and in drug
 CC screening techniques. The present sequence represents a cDNA encoding a
 CC novel human polypeptide of the invention.
 XX

Sequence 1252 BP; 302 A; 371 C; 266 G; 313 T; 0 other;
 SQ

Query Match 8.3%; Score 54.4; DB 22; Length 1552;
 Best Local Similarity 70.2%; Pred. No. 0.00024;
 Matches 73; Conservative 0; Mismatches 31; Indels 0; Gaps 0;

Oy 218 GTGGAAGAGCGCTTCAGTACTGACCAACATCGCCCTTGGGCTTGGCCT 277
 ||||| 11 11 ||||| 11 11 ||||| 11 11 ||||| 11 11 |||||
 Db 291 GTTGATGACGATGCTTAAGTCTTTAAACCAACCGCTTCTGCTTCAGGCT 350

Oy 278 CATGACCATCGCATGACACTGACTGCTACACAGAG 321
 ||||| 11 11 ||||| ||||| 1111
 Db 351 GATGACCATGCTGTGGACCGACTATGTGCTTACTCCAGAG 394

RESULT 8
 AA251628
 ID AA251628 standard; cDNA; 1478 BP.
 XX
 AC AA251628;
 DT 21-JUN-2000 (first entry)
 XX
 DE Human membrane channel protein-12 (MECHP-12) cDNA.
 XX
 KM Membrane channel protein-12; MECHP-12; diagnosis; treatment; lymphoma;
 KM cell proliferative disorder; bursts; atherosclerosis; cancer; sarcoma;
 KM inflammatory disorder; AIDS; Addison's disease; cystic fibrosis; asthma;
 KM diabetes mellitus; osmoregulatory disorder; diarrhoea; renal failure;
 KM muscular disorder; myocarditis; Duchenne's muscular dystrophy; noctropic;
 KM cardiovascular disorder; hypertension; bronchitis; vasculitis; cardiant;
 KM neurological disorder; Alzheimer's disease; Parkinson's disease; human;
 KM Huntington's disease; antiarteriosclerotic; hepatotropic; cytoskeletal;
 KM anti-HIV; antianaemic; neuroprotective; immunomodulator; antidiabetic;
 KM hypotensive; vasotropic; antihistaminic; antiinflammatory; antidepressant;
 KM anticonvulsant; thrombolytic; antiParkinsonian; immunostimulant; ss.
 XX
 OS Homo sapiens.
 FH Key location/Qualifiers
 FT CDS 364..1335
 FT /*tag= a
 FT /product= "MECHP-12"
 FT 994..1041
 FT /*tag= b
 FT /bound_moiety= "Primer or Probe"
 PN W0200012711-A2.
 PD 09-MAR-2000.
 XX
 PF 02-SEP-1999; 99WO-US20468.
 XX
 PR 02-SEP-1998; 98US-0145815.

XX 06-SEP-1999; 99WO-GB02945.
PF
XX
PR 08-SEP-1998; 98GB-0019589.
XX
XX
PA (SMIK) SMITHKLINE BEECHAM PLC.
XX
PI Duckworth DM, Hayes PD;
XX
DR WPI; 2000-256977/22.
P-PSDB: AAY84374.
XX
XX
PT CACNGLIKE polynucleotides and polypeptides, useful in diagnostic assays
and for treating conditions such as Alzheimer's -
XX
PS Claim 4; Page 29; 33pp; English.
XX
XX The present sequence encodes a putative human neuronal voltage-gated
calcium channel gamma 2 and gamma 3 subunits, designated CACNGLIKE2
polypeptides. The CACNGLIKE2 polynucleotide and polypeptide are
useful for treating neurological disorders, epilepsies, stroke, head
trauma, migraine, affective disorders including depression and anxiety,
schizophrenia, neurodegenerative disorders including Alzheimer's disease,
cognitive disorders, pain and cancer. They may also be used to configure
screening methods for detecting the effect of added compounds on the
production of mRNA in cells. The polypeptides may also be used as
vaccines to induce an immunological response in mammals.
XX
XX Sequence 948 BP; 234 A; 273 C; 218 G; 223 T; 0 other;
Query Match 7.9%; Score 52; DB 21; Length 948;
Best Local Similarity 65.5%; Pred. No. 0.00091;
Matches 76; Conservative 0; Mismatches 40; Indels 0; Gaps 0;
OY 218 GTGTGAAAAGGCGCTTCAGTACTACTGACACGACGCGGCGCTTTGGCCT 277
DB 9 GTGTGACAGAGGTATCCAGATGTGTGATCCACACTGTAGAGCGCTTTGCCGCTTTAGTTT 68
OY 278 CATGACCATGCGCATCAGCATGACTGCTGCTTACACAGAGCTCTCATCTGCA 333
DB 69 AATGACCATTTGCGAGTGGCAGCGAGCTACTGTTATTTCCAGAGGTGTGACGGA 124
RESULT 13
ABA09004 standard; cDNA; 1383 BP.
XX
AC ABA09004;
XX
DT 11-JAN-2002 (first entry)
XX
DE Human voltage gated Cl channel subunit homologue cDNA, SEQ ID NO:780.
XX
XX Human: cytokine; cell proliferation; tissue growth; immunomodulator; growth factor;
haematopoiesis regulation; tissue growth; immunomodulator; activin;
inhibin; chemokinesis; chemokinesis; thrombolytic; oncogenesis;
proliferation; metastasis; cancer; tumour; haematopoietic disorder;
myeloid cell disorder; lymphoid cell disorder; asthma; arthritis;
chronic inflammatory condition; proliferative retinopathy;
atherosclerosis; coronary heart disease; arterial ischaemia;
bone disorder; osteoporosis; vascular growth disorder;
tissue regeneration; wound healing; infection; immune disorder;
cell culture; drug screening; gene therapy; antiinflammatory;
antiallergic; antiallergic; haemostatic; antiallergic;
cytostatic; osteopathic; vasotropic; cardiac; virucide; antibacterial;
antifungal; vulnery; antitumor; ss.
XX
OS Homo sapiens.
XX
PN WO200157188-A2.
XX
XX 09-AUG-2001.
PD
XX

PF 05-FEB-2001; 2001WO-US03800.
XX
XX 03-FEB-2000; 2000US-0496914.
PR 27-APR-2000; 2000US-0560875.
XX
XX (HYSE-) HYSEQ INC.
XX
PI Tang YT, Liu C, Dirmannac RT;
XX
DR WPI; 2001-457740/49.
P-PSDB: ABB11760.
XX
XX Human proteins and DNA encoding sequences useful for preventing,
treating or ameliorating a medical condition in a mammalian subject
e.g. arthritis and cancer -
XX
XX Claim 1; Page 691-692; 1963pp; English.
XX
XX Sequences ABB10981-ABB12330 represent 1350 novel human polypeptides, and
sequences ABA08225-ABA09574 represent nucleic acids encoding them. The
invention also relates to vectors and recombinant host cells comprising a
nucleotide of the invention, methods of producing the novel polypeptides,
antibodies against the polypeptides, methods of detecting the nucleotides
or polypeptides in a sample, and methods of identifying compounds which
bind to polypeptides of the invention. Although novel, many of the
polypeptides of the invention have homology to known proteins, thereby
giving an insight into their probable biological activities, and hence
potential therapeutic applications. The polypeptides of the invention may
have various activities, including cytokine, cell proliferation or cell
differentiation activities, stem cell growth factor activity;
haematopoiesis regulatory activity; tissue growth activity;
immunomodulatory activity; activin- or inhibin-related activities;
chemotactic or chemokinetic activities; haemostatic, thrombotic or
thrombolytic activities; receptor or ligand activities; or may be
involved in oncogenesis, cancer cell proliferation or metastasis.
Depending on their biological activities, polypeptides and nucleotides of
the invention are useful for preventing, treating or ameliorating medical
conditions, e.g., by protein or gene therapy. Such conditions include
cancers, haematopoietic disorders (e.g., myeloid or lymphoid cell
disorders), chronic inflammatory conditions (e.g., asthma or arthritis),
proliferative retinopathy, atherosclerosis, coronary heart disease,
arterial ischaemia, bone disorders (e.g., osteoporosis), and abnormal
vascular growth. Polypeptides involved with tissue regeneration and
repair (or nucleic acids encoding them) may be used to promote wound
healing (e.g., of burns, incisions and ulcers), while those with
CC immunomodulatory activities may be used in the treatment of viral,
bacterial and fungal infections in addition to immune disorders.
CC polypeptides with growth factor activity may be used in cell cultures to
promote cell growth. For example, such polypeptides may be used to
manipulate stem cells in culture to give rise to neuroepithelial cells
that can be used to augment or replace cells damaged by illness,
CC autoimmune disease or accidental damage. The polypeptides and nucleotides
CC may also be used in the diagnosis of the above conditions, and in drug
screening techniques. The present sequence represents a cDNA encoding a
novel human polypeptide of the invention.
XX
XX Sequence 1383 BP; 336 A; 407 C; 341 G; 299 T; 0 other;
Query Match 7.9%; Score 52; DB 22; Length 1383;
Best Local Similarity 65.5%; Pred. No. 0.001;
Matches 76; Conservative 0; Mismatches 40; Indels 0; Gaps 0;
OY 218 GTGTGAAAAGGCGCTTCAGTACTACTGACACGACGCGGCGCTTTGGCCT 277
DB 429 GTGTGACAGAGGTATCCAGATGTGTGATCCACACTGTAGAGCGCTTTGCCGCTTTAGTTT 488
OY 278 CATGACCATGCGCATCAGCATGACTGCTGCTTACACAGAGCTCTCATCTGCA 333
DB 489 AATGACCATTTGCGAGTGGCAGCGAGCTACTGTTATTTCCAGAGGTGTGACGGA 544
RESULT 14
AAC77216

ID AAC77216 standard; cDNA; 1854 BP.
 XX AAC77216;
 XX
 DT 08-FEB-2001 (first entry)
 DE Human ORFX ORF2771 polynucleotide sequence SEQ ID NO:5541.
 XX
 KW Human: open reading frame; ORFX; detection: cytostatic; hepatotropic;
 KW vulnery; antiparkinsonian; nocrotropic; neuroprotective;
 KW anticonvulsant; osteopethic; antilarthritic; immunosuppressant; cardiant;
 KW immunostimulant; thrombolytic; coagulant; vasotropic; antidiabetic;
 KW hypotensive; dermatological; immunosuppressive; antinflammatory;
 KW antiviral; antibacterial; antifungal; antirheumatic; antithyroid;
 KW antianemic; gene therapy; cancer; proliferative disorder; hypertension;
 KW neurodegenerative disorder; osteoarthritis; graft vs host disease;
 KW cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; AIDS;
 KW cholesterol ester storage; systemic lupus erythematosus; infection;
 KW severe combined immunodeficiency; malaria; autoimmune disorder; asthma;
 KW allergy; aplastic anaemia; nocturnal hemoglobinuria; burn; wound;
 KW bone damage; cartilage damage; antiinflammatory disease; coagulation;
 KW thrombosis; contraceptive; ss.
 KW
 XX Homo sapiens.
 OS
 XX
 PN WO200058473-A2.
 PD 05-OCT-2000.
 XX
 PF 31-MAR-2000; 2000WO-US08621.
 XX
 PR 31-MAR-1999; 99US-0127607.
 PR 02-APR-1999; 99US-0127636.
 PR 03-APR-1999; 99US-0127728.
 PR 30-MAR-2000; 2000US-0540763.
 XX
 PA (CURA-) CURAGEN CORP.
 PI Shinkets RA, Leach M;
 DR WPI: 2000-602362/57.
 P-PSDB: AAB43007.
 XX
 PT Novel nucleic acids and peptides derived from open reading frame X.
 PT useful for treating e.g. cancers, proliferative disorders,
 PT neurodegenerative disorders and cardiovascular disease -
 XX
 PS Claim 5; Page 4724-4725; 5507pp; English.
 XX
 CC AAC74446 to AAC77606 encode the proteins given in AAB40237 to AAB43397,
 CC which represent the human ORFX open reading frames 1 to 3161. The ORFX
 CC sequences have activities such as: cytostatic; hepatotropic; vulnery;
 CC antiparkinsonian; antiparkinsonian; nocrotropic; neuroprotective;
 CC osteopethic; anticonvulsant; antilarthritic; immunosuppressant;
 CC immunostimulant; cardiant; thrombolytic; coagulant; vasotropic;
 CC antidiabetic; hypotensive; dermatological; immunosuppressive;
 CC antiinflammatory; antibacterial; antiviral; antifungal; antirheumatic;
 CC antithyroid; and antianemic. The sequences can be used for determining
 CC the presence of or predisposition to, or preventing or treating
 CC pathological conditions associated with an ORFX-associated disorder. The
 CC nucleic acids can be used to express ORFX proteins in gene therapy
 CC vectors. The proteins and nucleic acids may be used to treat cancers,
 CC proliferative disorders, neurodegenerative disorders, osteoarthritis,
 CC graft vs host disease, cardiovascular disease, diabetes mellitus,
 CC hypertension, hypothyroidism, cholesterol ester storage, systemic lupus
 CC erythematosus, severe combined immunodeficiency (SCID), AIDS, viral,
 CC bacterial or fungal infection, malaria, autoimmune disorders, asthma,
 CC allergies, aplastic anaemia, burns, wounds, bone and cartilage damage,
 CC nocturnal hemoglobinuria, antiinflammatory disease; to enhance
 CC coagulation; to inhibit thrombosis; and as a contraceptive.
 CC
 XX Sequence 1854 BP; 460 A; 549 C; 414 G; 429 T; 2 other;

Query Match 7.9%; Score 52; DB 21; Length 1854;
 Best local similarity 65.5%; Pred. No. 0.0011;
 Matches 76; Conservative 0; Mismatches 40; Indels 0; Gaps 0;
 OY 218 GTGTGAAAGGCGTTAGTACTGACGACACATCGCGCCCTTGGGCTT 277
 DB 354 GTGTACAGAGGTATTCAGATGTTGATCACCACCTGAGAGCCTTGGCGCTT 413
 OY 278 CATGACCATCGCATCAGACTGACTGCTGTACACAGAGCTTCATTCGA 333
 DB 414 AATGACCATGTCAGTGGGACGAGCTACTGTTATATTCAGAGGTGTGTGACGA 469
 RESULT 15
 ID AAV55831/C
 ID AAV55831 standard; DNA; 799 BP.
 XX
 AC AAV55831;
 XX
 DT 18-NOV-1998 (first entry)
 XX
 DE Nucleotide sequence of the stabilising sequence-encoding insert.
 XX
 KW Fusion protein; stabilising polypeptide; proteolytic degradation;
 KW resistance; half-life; autoimmune disease; inflammation; nitro drug;
 KW IkappaB regulator protein; inflammatory bowel disease; in vivo imaging;
 KW nitroreductase protein; enzyme therapy; prodrg therapy; protease;
 KW cancer; pathological condition; ss.
 KW
 XX Epstein-barr virus.
 OS
 XX
 PN WO9822577-A1.
 PD 28-MAY-1998.
 XX
 PF 17-NOV-1997; 97WO-1B01508.
 XX
 PR 25-JUN-1997; 97US-0048945.
 PR 15-NOV-1996; 96US-0030986.
 XX
 PA (MASU/) MASUCCI M G.
 PI Masucci MG;
 DR WPI: 1998-312463/27.
 XX
 PT New fusion proteins resistant to proteolytic degradation -
 PT comprising a core protein with a stabilising polypeptide comprising
 PT a peptide sequence containing glycine repeats
 XX
 PS Disclosure; Fig 4B; 120pp; English.
 XX
 CC This is a nucleotide sequence of the stabilising sequence-encoding
 CC insert. The invention provides a method for increasing the resistance
 CC of a core protein to proteolytic degradation that comprises linking or
 CC inserting onto or into the core protein a stabilising polypeptide of
 CC formula (Gly)nX(Gly)mY(Gly)pZn where Glya, Glyb, Glyc are 1-6
 CC sequential Gly residues and X, Y, Z are Ala, Ser, Val, Ile, Leu, Met,
 CC Phe, Pro or Thr and n can be anything between 1-66. X, Y and Z need not
 CC be identical from n repeat to n repeat. Alternatively a nucleic acid
 CC encoding the stabilising polypeptide can be linked onto or inserted into
 CC a nucleic acid encoding a core protein. The fusion proteins of the
 CC invention are more resistant to degradation by proteases and, thus, have
 CC a longer half-life than the unfused core protein. The products can be
 CC used for treating autoimmune diseases, cancer and inflammation. In
 CC particular, the core protein may be an IkappaB regulator protein for the
 CC treatment of inflammatory bowel disease, or a nitroreductase protein
 CC which can activate nitro drugs in enzyme/prodrug therapy to treat cancer
 CC or other pathological conditions. The fusion proteins can also be used in
 CC diagnostic methods such as in vivo imaging.
 CC
 XX Sequence 799 BP; 201 A; 106 C; 479 G; 13 T; 0 other;

Query Match 6.5%; Score 42.8; DB 19; Length 799;
Best Local Similarity 58.7%; Pred. No. 0.21;
Matches 74; Conservative 0; Mismatches 52; Indels 0; Gaps 0;

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DB 740 CTGCACCTTCGCTCGACGACACCTGCTGCGCCCGCCCGCCCTCGGCCCTTGAG 681
QY 73 GCGCCCGACCTTCGCTGCTGCTGATCCCGCCAGCGCGCGACGCGCCCGCTCGCG 132
DB 680 CCGCTGCTGCTCGCGCCCGCTGCGCCCGCTGCTGCGCCCGCTGCGCCCGCTGCTG 621
QY 133 TCGCCC 138
DB 620 CTGCCC 615

Search completed: February 9, 2003, 18:52:19
Job time : 229 secs

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: February 9, 2003, 18:47:48 : Search time 58 Seconds
(Without alignments)
5361.137 Million cell updates/sec

Title: US-10-060-066-2

Perfect score: 656
Sequence: 1 tatggtctactctgcacct.....tgtattttattttcttcttg 656

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 408267 seqs, 237001491 residues

Total number of hits satisfying chosen parameters: 816534

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

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- 2: /cgn2_6/ptodata/2/pubpna/PCRT_NEW_PUB.seq:*
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- 9: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
- 10: /cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq:*
- 11: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
- 12: /cgn2_6/ptodata/2/pubpna/US10_PUBCOMB.seq:*
- 13: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
- 14: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	86.4	13.2	984	10	US-09-883-483-1
2	40	6.1	1152	10	US-09-765-205-43
3	39.8	6.1	1377	9	US-09-944-413-41
4	39.8	6.1	1377	9	US-09-944-403-41
5	39.8	6.1	1377	9	US-09-944-896-41
6	39.8	6.1	1377	9	US-09-944-944-41
7	39.8	6.1	1377	9	US-09-944-907-41
8	39.8	6.1	1377	9	US-09-944-929-41
9	39.8	6.1	1377	9	US-10-028-072-361
10	39.8	6.1	1377	9	US-10-121-049-361
11	39.8	6.1	1377	9	US-10-123-904-361
12	39.8	6.1	1377	9	US-10-140-470-361
13	39.8	6.1	1377	10	US-09-866-028-41
14	39.8	6.1	1377	10	US-09-944-457-41
15	39.8	6.1	1377	10	US-09-944-457-41
16	39.8	6.1	1377	10	US-09-945-587-41
17	39.8	6.1	1377	10	US-09-945-015-41
18	39.8	6.1	1377	10	US-09-944-396-41
19	39.8	6.1	1377	10	US-09-944-097-41

C	20	39.8	6.1	1377	10	US-09-944-432-41	Sequence 41, Appl
C	21	39.8	6.1	1377	10	US-09-943-762-41	Sequence 41, Appl
C	22	39.8	6.1	1377	10	US-09-944-654-41	Sequence 41, Appl
C	23	39.8	6.1	1377	10	US-09-943-851A-41	Sequence 41, Appl
C	24	39.8	6.0	15231	9	US-10-095-407-16	Sequence 1, Appl
C	25	39.4	6.0	437	9	US-09-960-352-12835	Sequence 12835, A
C	26	39.4	6.0	4257	9	US-09-825-288A-1	Sequence 1, Appl
C	27	39.2	6.0	1065	10	US-09-804-682-33	Sequence 33, Appl
C	28	37.8	5.8	43058	10	US-09-954-456-292	Sequence 292, App
C	29	37.8	5.8	43058	10	US-09-954-456-529	Sequence 529, App
C	30	37.8	5.8	43058	10	US-09-880-107-3950	Sequence 3950, Ap
C	31	37.2	5.7	468	10	US-09-864-761-2321	Sequence 2321, Ap
C	32	37	5.6	1064	10	US-09-804-682-29	Sequence 29, Appl
C	33	37	5.6	53522	9	US-09-904-968A-1	Sequence 1, Appl
C	34	36.6	5.6	1614	9	US-09-976-740-45	Sequence 45, Appl
C	35	36.6	5.6	1614	12	US-10-023-529-45	Sequence 45, Appl
C	36	36.6	5.6	1614	12	US-10-023-523-45	Sequence 45, Appl
C	37	36.6	5.6	2608	10	US-09-739-254-16	Sequence 16, Appl
C	38	36.6	5.6	2608	10	US-09-904-615-16	Sequence 16, Appl
C	39	36.6	5.6	5983	10	US-09-799-875-4	Sequence 4, Appl
C	40	36.6	5.6	12425	9	US-09-976-740-50	Sequence 50, Appl
C	41	36.6	5.6	12425	12	US-10-023-529-50	Sequence 50, Appl
C	42	36.6	5.6	12425	12	US-10-023-523-50	Sequence 50, Appl
C	43	36.4	5.5	3203	10	US-09-880-107-2164	Sequence 2164, Ap
C	44	36.4	5.5	14800	10	US-09-954-456-1601	Sequence 1601, Ap
C	45	36.2	5.5	485	9	US-10-004-717-59	Sequence 59, Appl

ALIGNMENTS

RESULT 1
US-09-883-483-1
: Sequence 1, Application US/09883483
: Patent No. US20020128454A1
: GENERAL INFORMATION:
: APPLICANT: DUCKWORTH, David Malcolm
: TITLE OF INVENTION: NOVEL COMPOUNDS
: FILE REFERENCE: GP-30180-D1
: CURRENT APPLICATION NUMBER: US/09/883,483
: PRIOR FILING DATE: 2001-06-18
: PRIOR APPLICATION NUMBER: UK 9819592.8
: PRIOR FILING DATE: 1998-09-08
: PRIOR APPLICATION NUMBER: 09/392,014
: NUMBER OF SEQ ID NOS: 4
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 1
: LENGTH: 984
: TYPE: DNA
: ORGANISM: HOMO SAPIENS
US-09-883-483-1

Query Match	13.2%	Score 86.4:	DB 10:	Length 984:
Best Local Similarity	66.8%	Pred. No. 2.4e-14:		
Matches 123:	Conservative	0:	Mismatches 61:	Indels 0:
Gaps 0:				
QY	214	TGTGTGTGAAGAAGCGCTTCAGGTACTACTGACCACTGCGGCGCTTGTG	273	
DB	5	TGCATGCGACCGGCGGTGCAAGATGCTGTCGACCAAGCGGAGCGCTTGC	64	
QY	274	GCTTCATGACCATGCCATGACGACTGACTGCTTACCAAGAGCTTACTGCA	333	
DB	65	CGCTCATGCGCATGCGCTGCGACCGCACTGCTTACTCCAGCGGACATTCGA	124	
QY	334	ACACACCACTGACAGCAGTATGACGACCAACCCACTGCGGCGGAGTGGCTCT	393	
DB	125	ACGGACCACTGACATGACGACGCGGCGGCGGCGGCGGCGGCACTCA	184	
QY	394	CCGA 397		
DB	185	CCCA 188		


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RESULT 2
US-09-765-205-43
: Sequence 403, Application US/09765205
: Patent No. US20020034800A1
: GENERAL INFORMATION:
: APPLICANT: Cao, Li
: TITLE OF INVENTION: BONE MARROW SECRETED PROTEINS AND POLYNUCLEOTIDES
: FILE REFERENCE: 1458.004/200130.449
: CURRENT APPLICATION NUMBER: US/09/765,205
: CURRENT FILING DATE: 2001-01-17
: PRIOR APPLICATION NUMBER: US/09/212,440
: PRIOR FILING DATE: 1998-12-16
: NUMBER OF SEQ ID NOS: 46
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 43
: LENGTH: 1152
: TYPE: DNA
: ORGANISM: human
US-09-765-205-43

Query Match      6.1%; Score 40; DB 10; Length 1152;
Best Local Similarity 53.9%; Pred. No. 0.14;
Matches 82; Conservative 0; Mismatches 70; Indels 0; Gaps 0;

Qy 22 CGCCTCTGCAGCCACCTGCTCGTCCGCGCCGCGCCCTCTGCGCCCTTGAGGCCGCCCGCAG 81
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Db 116 CGCCTGAGACAGCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCT 175
Qy 82 CTTCGCGCTGCTGCTGATCCCCCAGCGCGCGCGCGCGCGCGCGCGCTCGCTGCGCGCGT 141
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 176 CCCCTCCCGCGCGCGCTGCTGCTCCCGAGGCGGCGCGCGCGCGCTCCAGCCCGCAGCCCGCC 235
Qy 142 GGTGCGCCAGCGCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGT 173
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Db 236 GGGGTCCCTGGGGGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGT 267

RESULT 3
US-09-944-413-41/c
: Sequence 41, Application US/09944413
: Patent No. US2002015600A1
: GENERAL INFORMATION:
: APPLICANT: Baker, Kevin
: APPLICANT: Botstein, David
: APPLICANT: Eaton, Dan
: APPLICANT: Ferrara, Napoleone
: APPLICANT: Filvaroff, Ellen
: APPLICANT: Gerltsen, Mary
: APPLICANT: Goddard, Audrey
: APPLICANT: Godowski, Paul
: APPLICANT: Grimaldi, Christopher
: APPLICANT: Gurney, Austin
: APPLICANT: Hillan, Kenneth
: APPLICANT: Kljavin, Ivar
: APPLICANT: Napier, Mary
: APPLICANT: Roy, Margaret
: APPLICANT: Tumas, Daniel
: APPLICANT: Wood, William
: TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
: FILE REFERENCE: P2548P1C1
: CURRENT APPLICATION NUMBER: US/09/944,413
: CURRENT FILING DATE: 2001-09-26
: PRIOR APPLICATION NUMBER: 09/866,028
: PRIOR FILING DATE: 2001-05-25
: PRIOR APPLICATION NUMBER: 60/067,411
: PRIOR FILING DATE: December 3, 1997
: PRIOR APPLICATION NUMBER: 60/069,334
: PRIOR FILING DATE: December 11, 1997
: PRIOR APPLICATION NUMBER: 60/069,335
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: PRIOR APPLICATION NUMBER: 60/069,278
: PRIOR FILING DATE: December 11, 1997
: PRIOR APPLICATION NUMBER: 60/069,425
: PRIOR FILING DATE: December 12, 1997
: PRIOR APPLICATION NUMBER: 60/069,696
: PRIOR FILING DATE: December 16, 1997
: PRIOR APPLICATION NUMBER: 60/069,694
: PRIOR FILING DATE: December 16, 1997
: PRIOR APPLICATION NUMBER: 60/069,702
: PRIOR FILING DATE: December 16, 1997
: PRIOR APPLICATION NUMBER: 60/069,870
: PRIOR FILING DATE: December 17, 1997
: PRIOR APPLICATION NUMBER: 60/069,873
: PRIOR FILING DATE: December 17, 1997
: PRIOR APPLICATION NUMBER: 60/068,017
: PRIOR FILING DATE: December 17, 1997
: PRIOR APPLICATION NUMBER: 60/070,440
: PRIOR FILING DATE: January 5, 1998
: PRIOR APPLICATION NUMBER: 60/074,086
: PRIOR FILING DATE: February 9, 1998
: PRIOR APPLICATION NUMBER: 60/074,092
: PRIOR FILING DATE: February 9, 1998
: PRIOR APPLICATION NUMBER: 60/075,945
: PRIOR FILING DATE: February 25, 1998
: PRIOR APPLICATION NUMBER: 60/112,850
: PRIOR FILING DATE: December 16, 1998
: PRIOR APPLICATION NUMBER: 60/113,296
: PRIOR FILING DATE: December 22, 1998
: PRIOR APPLICATION NUMBER: 60/146,222
: PRIOR FILING DATE: July 28, 1999
: PRIOR APPLICATION NUMBER: PCT/US98/19330
: PRIOR FILING DATE: September 16, 1998
: PRIOR APPLICATION NUMBER: PCT/US98/25108
: PRIOR FILING DATE: December 1, 1998
: PRIOR APPLICATION NUMBER: 09/216,021
: PRIOR FILING DATE: December 16, 1998
: PRIOR APPLICATION NUMBER: 09/218,517
: PRIOR FILING DATE: December 22, 1998
: PRIOR APPLICATION NUMBER: 09/254,311
: PRIOR FILING DATE: March 3, 1999
: PRIOR APPLICATION NUMBER: PCT/US99/12252
: PRIOR FILING DATE: June 22, 1999
: PRIOR APPLICATION NUMBER: PCT/US99/21090
: PRIOR FILING DATE: September 15, 1999
: PRIOR APPLICATION NUMBER: PCT/US99/28409
: PRIOR FILING DATE: No. US2002015600A1eember 30, 1999
: PRIOR APPLICATION NUMBER: PCT/US99/28313
: PRIOR FILING DATE: No. US2002015600A1eember 30, 1999
: PRIOR APPLICATION NUMBER: PCT/US99/28301
: PRIOR FILING DATE: December 1, 1999
: PRIOR APPLICATION NUMBER: PCT/US99/30095
: PRIOR FILING DATE: December 16, 1999
: PRIOR APPLICATION NUMBER: PCT/US00/03565
: PRIOR FILING DATE: February 11, 2000
: PRIOR APPLICATION NUMBER: PCT/US00/04414
: PRIOR FILING DATE: February 22, 2000
: PRIOR APPLICATION NUMBER: PCT/US00/05841
: PRIOR FILING DATE: March 2, 2000
: PRIOR APPLICATION NUMBER: PCT/US00/08439
: PRIOR FILING DATE: March 30, 2000
: PRIOR APPLICATION NUMBER: PCT/US00/14042
: PRIOR FILING DATE: May 22, 2000
: PRIOR APPLICATION NUMBER: PCT/US00/20710
: PRIOR FILING DATE: July 28, 2000
: PRIOR APPLICATION NUMBER: PCT/US00/32678
: PRIOR FILING DATE: December 1, 2000
: PRIOR APPLICATION NUMBER: PCT/US01/06520
: PRIOR FILING DATE: February 28, 2001
: NUMBER OF SEQ ID NOS: 120
: SEQ ID NO 41
: LENGTH: 1377
: TYPE: DNA
: ORGANISM: Homo Sapien
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	PRIOR APPLICATION NUMBER:	60/074,092	
	PRIOR FILING DATE:	February 9, 1998	
	PRIOR APPLICATION NUMBER:	60/075,945	
	PRIOR FILING DATE:	February 25, 1998	
	PRIOR APPLICATION NUMBER:	60/112,850	
	PRIOR FILING DATE:	December 16, 1998	
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	PRIOR APPLICATION NUMBER:	PCT/US98/19330	
	PRIOR FILING DATE:	September 16, 1998	
	PRIOR APPLICATION NUMBER:	PCT/US98/25108	
	PRIOR FILING DATE:	December 1, 1998	
	PRIOR APPLICATION NUMBER:	09/216,021	
	PRIOR FILING DATE:	December 16, 1998	
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	PRIOR FILING DATE:	March 3, 1999	
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	PRIOR FILING DATE:	September 15, 1999	
	PRIOR APPLICATION NUMBER:	PCT/US99/28409	
	PRIOR FILING DATE:	No. US20020165143A1ember 30, 1999	
	PRIOR APPLICATION NUMBER:	PCT/US99/28313	
	PRIOR FILING DATE:	No. US20020165143A1ember 30, 1999	
	PRIOR APPLICATION NUMBER:	PCT/US99/28301	
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	PRIOR APPLICATION NUMBER:	PCT/US99/30095	
	PRIOR FILING DATE:	December 16, 1999	
	PRIOR APPLICATION NUMBER:	PCT/US00/03565	
	PRIOR FILING DATE:	February 11, 2000	
	PRIOR APPLICATION NUMBER:	PCT/US00/04414	
	PRIOR FILING DATE:	February 22, 2000	
	PRIOR APPLICATION NUMBER:	PCT/US00/05841	
	PRIOR FILING DATE:	March 2, 2000	
	PRIOR APPLICATION NUMBER:	PCT/US00/08439	
	PRIOR FILING DATE:	March 30, 2000	
	PRIOR APPLICATION NUMBER:	PCT/US00/14042	
	PRIOR FILING DATE:	May 22, 2000	
	PRIOR APPLICATION NUMBER:	PCT/US00/20710	
	PRIOR FILING DATE:	July 28, 2000	
	PRIOR APPLICATION NUMBER:	PCT/US00/32678	
	PRIOR FILING DATE:	December 1, 2000	
	PRIOR APPLICATION NUMBER:	PCT/US01/06520	
	PRIOR FILING DATE:	February 28, 2001	
	NUMBER OF SEQ ID NOS:	120	
	SEQ ID NO:	41	
	LENGTH:	1377	
	TYPE:	DNA	
	ORGANISM:	Homo Sapien	
	US-09-944-403-41		
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Best Local Similarity	56.5%;	Pred. No. 0.17;	
Matches	74;	Conservative	0; Mismatches 57; Indels 0; Gaps 0;
OY	37	CTGCTCGCTGCCCCCGGGCCCTGTGAGCCCTTGAGGCCCCCACTTCTGCTTGTGCTG	96
Db	479	CTCCTCGGGGCGCCCGGGGTCCCTTCAGATGCACGCGCATGTCGCGCTCCCGCCCTCGCCTT	420
OY	97	TGATGCCCCCAGCGCCCGGACAGGCGCCGCTGCGCGCCCGGGTGGTGGTGGCACAGGCGCC	156
Db	419	TCTCTTCGCGAGACCCCGGGCGCGCGCTGCGGCGCGCTCGGCGCATTCGCGCGCGCGCAAGC	360
OY	157	CCCGGTTGCCA	167
Db	359	CCTGGCTGCCA	349

US-09-944-896-41/C
Sequence 41, Application US/09944896
Patent No. US20020168715A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin
APPLICANT: Botstein, David
APPLICANT: Eaton, Dan
APPLICANT: Ferrara, Napoleone
APPLICANT: Filvaroff, Ellen
APPLICANT: Gerritsen, Mary
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul
APPLICANT: Grimaldi, Christopher
APPLICANT: Gurney, Austin
APPLICANT: Hillan, Kenneth
APPLICANT: Kijavlin, Ivar
APPLICANT: Napier, Mary
APPLICANT: Roy, Margaret
APPLICANT: Tumas, Daniel
APPLICANT: Wood, William
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P2548P1C1
CURRENT APPLICATION NUMBER: US/09/944, 896
CURRENT FILING DATE: 2001-08-31
PRIOR APPLICATION NUMBER: 09/866, 028
PRIOR FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: 60/069, 334
PRIOR FILING DATE: December 11, 1997
PRIOR APPLICATION NUMBER: 60/069, 335
PRIOR FILING DATE: December 11, 1997
PRIOR APPLICATION NUMBER: 60/069, 278
PRIOR FILING DATE: December 11, 1997
PRIOR APPLICATION NUMBER: 60/069, 425
PRIOR FILING DATE: December 12, 1997
PRIOR APPLICATION NUMBER: 60/069, 696
PRIOR FILING DATE: December 16, 1997
PRIOR APPLICATION NUMBER: 60/069, 694
PRIOR FILING DATE: December 16, 1997
PRIOR APPLICATION NUMBER: 60/069, 702
PRIOR FILING DATE: December 16, 1997
PRIOR APPLICATION NUMBER: 60/069, 870
PRIOR FILING DATE: December 17, 1997
PRIOR APPLICATION NUMBER: 60/069, 873
PRIOR FILING DATE: December 17, 1997
PRIOR APPLICATION NUMBER: 60/068, 017
PRIOR FILING DATE: December 18, 1997
PRIOR APPLICATION NUMBER: 60/070, 440
PRIOR FILING DATE: January 5, 1998
PRIOR APPLICATION NUMBER: 60/074, 086
PRIOR FILING DATE: February 9, 1998
PRIOR APPLICATION NUMBER: 60/074, 092
PRIOR FILING DATE: February 9, 1998
PRIOR APPLICATION NUMBER: 60/075, 945
PRIOR FILING DATE: February 25, 1998
PRIOR APPLICATION NUMBER: 60/112, 850
PRIOR FILING DATE: December 16, 1998
PRIOR APPLICATION NUMBER: 60/113, 296
PRIOR FILING DATE: December 22, 1998
PRIOR APPLICATION NUMBER: 60/146, 222
PRIOR FILING DATE: July 28, 1999
PRIOR APPLICATION NUMBER: PCT/US98/19330
PRIOR FILING DATE: September 16, 1998
PRIOR APPLICATION NUMBER: PCT/US98/25108
PRIOR FILING DATE: December 1, 1998
PRIOR APPLICATION NUMBER: 09/216, 021
PRIOR FILING DATE: December 16, 1998
PRIOR APPLICATION NUMBER: 09/218, 517
PRIOR FILING DATE: December 22, 1998
PRIOR APPLICATION NUMBER: 09/254, 311
PRIOR FILING DATE: March 3, 1999
PRIOR APPLICATION NUMBER: PCT/US99/12252
PRIOR FILING DATE: June 22, 1999

PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR FILING DATE: September 15, 1999
PRIOR APPLICATION NUMBER: PCT/US99/28409
PRIOR FILING DATE: No. US20020168715A1ember 30, 1999
PRIOR APPLICATION NUMBER: PCT/US99/28313
PRIOR FILING DATE: No. US20020168715A1ember 30, 1999
PRIOR APPLICATION NUMBER: PCT/US99/28301
PRIOR FILING DATE: December 1, 1999
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR FILING DATE: December 16, 1999
PRIOR APPLICATION NUMBER: PCT/US00/03565
PRIOR FILING DATE: February 11, 2000
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: February 22, 2000
PRIOR APPLICATION NUMBER: PCT/US00/05841
PRIOR FILING DATE: March 2, 2000
PRIOR APPLICATION NUMBER: PCT/US00/08439
PRIOR FILING DATE: March 30, 2000
PRIOR APPLICATION NUMBER: PCT/US00/14042
PRIOR FILING DATE: May 22, 2000
PRIOR APPLICATION NUMBER: PCT/US00/20710
PRIOR FILING DATE: July 28, 2000
PRIOR APPLICATION NUMBER: PCT/US00/32678
PRIOR FILING DATE: December 1, 2000
PRIOR APPLICATION NUMBER: PCT/US01/06520
NUMBER OF SEQ ID NOS: 120
SEQ ID NO 41
LENGTH: 1377
TYPE: DNA
ORGANISM: Homo Sapien
US-09-944-896-41
Query Match 6.1%; Score 39.8; DB 9; Length 1377;
Best Local Similarity 56.5%; Pred. No. 0.17;
Matches 74; Conservative 0; Mismatches 57; Indels 0; Gaps 0;
QY 37 CTGCTGCTGCCCCCGCCCTGTGAGCCCTTGAGCCGCCACCTCTGCTGCTG 96
DB 479 CTCCTCGGGGCGCCGCGGTCCTCGAGGTCGCGGAGTCCCGCCTCCGCGCTGCTG 420
QY 97 TGATCCCCCAGCCCGCGGACGCGCCGCTGCGCTGCGCGGTCGCGGACGCGCC 156
DB 419 TCTCTCCCGGAGCCCGGCGCGCTGCGGCGCTGCGGCGCATGCGGCGCGGACG 360
QY 157 CCGGCTGCGCA 167
DB 359 CCTGCTGCGCA 349
RESULT 6
US-09-944-944-41/C
Sequence 41, Application US/09944944
Patent No. US20020173463A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin
APPLICANT: Botstein, David
APPLICANT: Eaton, Dan
APPLICANT: Ferrara, Napoleone
APPLICANT: Filvaroff, Ellen
APPLICANT: Gerritsen, Mary
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul
APPLICANT: Grimaldi, Christopher
APPLICANT: Gurney, Austin
APPLICANT: Hillan, Kenneth
APPLICANT: Kijavlin, Ivar
APPLICANT: Napier, Mary
APPLICANT: Roy, Margaret
APPLICANT: Tumas, Daniel
APPLICANT: Wood, William
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: ACIDS ENCODING THE SAME

```
FILE REFERENCE: P2548P1C1
CURRENT APPLICATION NUMBER: US/09/944,944
PRIOR APPLICATION NUMBER: 2001-09-26
PRIOR FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: 60/067,411
PRIOR FILING DATE: December 3, 1997
PRIOR APPLICATION NUMBER: 60/069,334
PRIOR FILING DATE: December 11, 1997
PRIOR APPLICATION NUMBER: 60/069,335
PRIOR FILING DATE: December 11, 1997
PRIOR APPLICATION NUMBER: 60/069,278
PRIOR FILING DATE: December 11, 1997
PRIOR APPLICATION NUMBER: 60/069,425
PRIOR FILING DATE: December 12, 1997
PRIOR APPLICATION NUMBER: 60/069,596
PRIOR FILING DATE: December 16, 1997
PRIOR APPLICATION NUMBER: 60/069,594
PRIOR FILING DATE: December 16, 1997
PRIOR APPLICATION NUMBER: 60/069,702
PRIOR FILING DATE: December 16, 1997
PRIOR APPLICATION NUMBER: 60/069,870
PRIOR FILING DATE: December 17, 1997
PRIOR APPLICATION NUMBER: 60/069,873
PRIOR FILING DATE: December 17, 1997
PRIOR APPLICATION NUMBER: 60/068,017
PRIOR FILING DATE: December 18, 1997
PRIOR APPLICATION NUMBER: 60/070,440
PRIOR FILING DATE: January 5, 1998
PRIOR APPLICATION NUMBER: 60/074,086
PRIOR FILING DATE: February 9, 1998
PRIOR APPLICATION NUMBER: 60/074,092
PRIOR FILING DATE: February 9, 1998
PRIOR APPLICATION NUMBER: 60/075,945
PRIOR FILING DATE: February 25, 1998
PRIOR APPLICATION NUMBER: 60/112,850
PRIOR FILING DATE: December 16, 1998
PRIOR APPLICATION NUMBER: 60/113,296
PRIOR FILING DATE: December 22, 1998
PRIOR APPLICATION NUMBER: 60/146,222
PRIOR FILING DATE: July 28, 1999
PRIOR APPLICATION NUMBER: PCT/US98/19330
PRIOR FILING DATE: September 16, 1998
PRIOR APPLICATION NUMBER: PCT/US98/25108
PRIOR FILING DATE: December 1, 1998
PRIOR APPLICATION NUMBER: 09/216,021
PRIOR FILING DATE: December 16, 1998
PRIOR APPLICATION NUMBER: 09/218,517
PRIOR FILING DATE: December 22, 1998
PRIOR APPLICATION NUMBER: 09/254,311
PRIOR FILING DATE: March 3, 1999
PRIOR APPLICATION NUMBER: PCT/US99/12252
PRIOR FILING DATE: June 22, 1999
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR FILING DATE: September 15, 1999
PRIOR APPLICATION NUMBER: PCT/US99/28409
PRIOR FILING DATE: No. US20020173463A1ember 30, 1999
PRIOR APPLICATION NUMBER: PCT/US99/28313
PRIOR FILING DATE: No. US20020173463A1ember 30, 1999
PRIOR APPLICATION NUMBER: PCT/US99/28301
PRIOR FILING DATE: December 1, 1999
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR FILING DATE: December 16, 1999
PRIOR APPLICATION NUMBER: PCT/US00/03565
PRIOR FILING DATE: February 11, 2000
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: February 22, 2000
PRIOR APPLICATION NUMBER: PCT/US00/05841
PRIOR FILING DATE: March 2, 2000
PRIOR APPLICATION NUMBER: PCT/US00/08439
PRIOR FILING DATE: March 30, 2000
PRIOR APPLICATION NUMBER: PCT/US00/14042
PRIOR FILING DATE: May 22, 2000

PRIOR APPLICATION NUMBER: PCT/US00/20710
PRIOR FILING DATE: July 28, 2000
PRIOR APPLICATION NUMBER: PCT/US00/32678
PRIOR FILING DATE: December 1, 2000
PRIOR APPLICATION NUMBER: PCT/US01/06520
PRIOR FILING DATE: February 28, 2001
NUMBER OF SEQ ID NOS: 120
SEQ ID NO 41
LENGTH: 1377
TYPE: DNA
ORGANISM: Homo Sapien
US-09-944-944-41

Query Match
Best Local Similarity 56.1%; Score 39.8; DB 9; Length 1377;
Matches 74; Conservative 0; Mismatches 57; Indels 0; Gaps 0;

QY 37 CTGCTGCTGCCCCGCGCCCTCTGCGCCCTTGAGCGCCCAAGCTTCTGCTGTGCTG 96
Db 479 CTCTCGCGGCGCGCGGCTCCCTCGAGGTCCGCGAGTCCGCGCTCCGCGCTGCTT 420
QY 97 TGATCCCCCAAGCGCGCGCGCCCTCGGCTGCCCCGGTGTGCGCCAGGCCC 156
Db 419 TCTCTCCGAGCGCGCGCGCGCGCTGCGCGCGCTCGCGCGCTCGCGCGCGCAAGC 360
QY 157 CCGGTTGCCA 167
Db 359 CCGGCTGCCA 349

RESULT 7
US-09-944-907-41/C
Sequence 41, Application US/09944907
Publication No. US20020198147A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin
APPLICANT: Botstein, David
APPLICANT: Eaton, Dan
APPLICANT: Ferrara, Napoleone
APPLICANT: Filvaroff, Ellen
APPLICANT: Gerritsen, Mary
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul
APPLICANT: Grimaldi, Christopher
APPLICANT: Gurney, Austin
APPLICANT: Hillan, Kenneth
APPLICANT: Kilgavin, Ivar
APPLICANT: Napier, Mary
APPLICANT: Roy, Margaret
APPLICANT: Tumas, Daniel
APPLICANT: Wood, William
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P2548P1C1
CURRENT APPLICATION NUMBER: US/09/944,907
PRIOR FILING DATE: 2001-08-31
PRIOR APPLICATION NUMBER: 09/866,028
PRIOR FILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 120
SEQ ID NO 41
LENGTH: 1377
TYPE: DNA
ORGANISM: Homo Sapien
US-09-944-907-41

Query Match
Best Local Similarity 56.1%; Score 39.8; DB 9; Length 1377;
Matches 74; Conservative 0; Mismatches 57; Indels 0; Gaps 0;

QY 37 CTGCTGCTGCCCCGCGCCCTCTGCGCCCTTGAGCGCCCAAGCTTCTGCTGTGCTG 96
Db 479 CTCTCGCGGCGCGCGGCTCCCTCGAGGTCCGCGAGTCCGCGCTCCGCGCTGCTT 420
```

OY 97 TGAATCCCCAGCGCCGCGGCGCCGCTTCGCTGCCCCGGGTGTGGCCACAGCGCC 156
DB 419 TCTCTCCCGAGCGCCGCGGCGCGCTCGCGCCGATCGCGCCCGGCAAGC 360
OY 157 CCCGGTTGCCA 167
DB 359 CCTGGCTGCCA 349

RESULT 8

US-09-944-929-41/c

; Sequence 41, Application US/09944929

; Publication No. US20020197612A1

; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin

; APPLICANT: Botstein, David

; APPLICANT: Eaton, Dan

; APPLICANT: Ferrara, Napoleone

; APPLICANT: Filvaroff, Ellen

; APPLICANT: Gerltsen, Mary

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul

; APPLICANT: Grimaldi, Christopher

; APPLICANT: Gurney, Austin

; APPLICANT: Hillan, Kenneth

; APPLICANT: Kijavlin, Ivar

; APPLICANT: Napier, Mary

; APPLICANT: Roy, Margaret

; APPLICANT: Tumas, Daniel

; APPLICANT: Wood, William

; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

; FILE REFERENCE: P2548P1C1

; CURRENT APPLICATION NUMBER: US/09/944,929

; CURRENT FILING DATE: 2001-08-31

; PRIOR APPLICATION NUMBER: 09/866,028

; PRIOR FILING DATE: 2001-05-25

; NUMBER OF SEQ ID NOS: 120

; SEQ ID NO 41

; LENGTH: 1377

; TYPE: DNA

; ORGANISM: Homo Sapien

US-09-944-929-41

Query Match 6.1%; Score 39.8; DB 9; Length 1377;

Best Local Similarity 56.5%; Pred. No. 0.17;

Matches 74; Conservative 0; Mismatches 57; Indels 0; Gaps 0;

OY 37 CTGCTGCGTCCGCGCCGCGCCCTCTGTGAGCCGCCAGCTTCTGCTGTGCTG 96
DB 479 CTCTCTGCGCGCCGCGGCTCCCTCGAGTCCGCGCACTCCGCGCTCCGCTT 420
OY 97 TGAATCCCCAGCGCGCGCGCGCTCCGCTGCGCGGTGCGCGCCACAGCGCC 156
DB 419 TCTCTCCCGAGCGCCGCGGCGCGCTCGCGCCGATCGCGCCCGGCAAGC 360
OY 157 CCCGGTTGCCA 167
DB 359 CCTGGCTGCCA 349

RESULT 9

US-10-028-072-361/c

; Sequence 361, Application US/10028072

; Publication No. US20030004311A1

; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.

; APPLICANT: Bersini, Maureen

; APPLICANT: DeForge, Laura

; APPLICANT: Desnoyers, Luc

; APPLICANT: Filvaroff, Ellen

; APPLICANT: Gao, Wei-Qiang

; APPLICANT: Gerltsen, Mary E.

APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Sherwood, Steven
APPLICANT: Smith, Victoria
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K
APPLICANT: Wood, William
APPLICANT: Zhang
; TITLE OF INVENTION:
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/028,072
; CURRENT FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 60/049911
; PRIOR FILING DATE: 1997-06-18
; PRIOR APPLICATION NUMBER: 60/056974
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059115
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059117
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059122
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059184
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059352
; PRIOR FILING DATE: 1997-09-19
; PRIOR APPLICATION NUMBER: 60/059588
; PRIOR FILING DATE: 1997-09-19
; PRIOR APPLICATION NUMBER: 60/059836
; PRIOR FILING DATE: 1997-09-24
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/062285
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/062814
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/062816
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063045
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063082
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/063127
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063327
; PRIOR FILING DATE: 1997-10-27
; PRIOR APPLICATION NUMBER: 60/063329
; PRIOR FILING DATE: 1997-10-27
; PRIOR APPLICATION NUMBER: 60/063550
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063561
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063704
; PRIOR FILING DATE: 1997-10-29
; PRIOR APPLICATION NUMBER: 60/063733
; PRIOR FILING DATE: 1997-10-29
; PRIOR APPLICATION NUMBER: 60/063735
; PRIOR FILING DATE: 1997-10-29
; PRIOR APPLICATION NUMBER: 60/063738
; PRIOR FILING DATE: 1997-10-29
; PRIOR APPLICATION NUMBER: 60/063755
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/064248
; PRIOR FILING DATE: 1997-11-03
; PRIOR APPLICATION NUMBER: 60/064809

;; PRIOR FILING DATE: 1997-11-07
;; PRIOR APPLICATION NUMBER: 60/065186
;; PRIOR FILING DATE: 1997-11-12
;; PRIOR APPLICATION NUMBER: 60/065846
;; PRIOR FILING DATE: 1997-11-17
;; PRIOR APPLICATION NUMBER: 60/066364
;; PRIOR FILING DATE: 1997-11-21
;; PRIOR APPLICATION NUMBER: 60/066453
;; PRIOR FILING DATE: 1997-11-24
;; PRIOR APPLICATION NUMBER: 60/066511
;; PRIOR FILING DATE: 1997-11-24
;; PRIOR APPLICATION NUMBER: 60/066770
;; PRIOR FILING DATE: 1997-11-24
;; PRIOR APPLICATION NUMBER: 60/069212
;; PRIOR FILING DATE: 1997-12-11
;; PRIOR APPLICATION NUMBER: 60/069278
;; PRIOR FILING DATE: 1997-12-11
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;; PRIOR FILING DATE: 1997-12-16
;; PRIOR APPLICATION NUMBER: 60/072320
;; PRIOR FILING DATE: 1998-01-23
;; PRIOR APPLICATION NUMBER: 60/073612
;; PRIOR FILING DATE: 1998-02-04
;; PRIOR APPLICATION NUMBER: 60/074086
;; PRIOR FILING DATE: 1998-02-09
;; PRIOR APPLICATION NUMBER: 60/074092
;; PRIOR FILING DATE: 1998-02-09
;; PRIOR APPLICATION NUMBER: 60/077791
;; PRIOR FILING DATE: 1998-03-12
;; PRIOR APPLICATION NUMBER: 60/078910
;; PRIOR FILING DATE: 1998-03-20
;; PRIOR APPLICATION NUMBER: 60/079294
;; PRIOR FILING DATE: 1998-03-25
;; PRIOR APPLICATION NUMBER: 60/079663
;; PRIOR FILING DATE: 1998-02-27
;; PRIOR APPLICATION NUMBER: 60/079728
;; PRIOR FILING DATE: 1998-03-27
;; PRIOR APPLICATION NUMBER: 60/080165
;; PRIOR FILING DATE: 1998-03-31
;; PRIOR APPLICATION NUMBER: 60/081203
;; PRIOR FILING DATE: 1998-04-09
;; PRIOR APPLICATION NUMBER: 60/081229
;; PRIOR FILING DATE: 1998-04-09
;; PRIOR APPLICATION NUMBER: 60/081695
;; PRIOR FILING DATE: 1998-04-14
;; PRIOR APPLICATION NUMBER: 60/081817
;; PRIOR FILING DATE: 1998-04-15
;; PRIOR APPLICATION NUMBER: 60/081818
;; PRIOR FILING DATE: 1998-04-15
;; PRIOR APPLICATION NUMBER: 60/082999
;; PRIOR FILING DATE: 1998-04-24
;; PRIOR APPLICATION NUMBER: 60/083322
;; PRIOR FILING DATE: 1998-04-28
;; PRIOR APPLICATION NUMBER: 60/083545
;; PRIOR FILING DATE: 1998-04-29
;; PRIOR APPLICATION NUMBER: 60/084600
;; PRIOR FILING DATE: 1998-05-07
;; PRIOR APPLICATION NUMBER: 60/084627
;; PRIOR FILING DATE: 1998-05-07
;; PRIOR APPLICATION NUMBER: 60/084637
;; PRIOR FILING DATE: 1998-05-07
;; PRIOR APPLICATION NUMBER: 60/085149
;; PRIOR FILING DATE: 1998-05-12
;; PRIOR APPLICATION NUMBER: 60/085323
;; PRIOR FILING DATE: 1998-05-13
;; PRIOR APPLICATION NUMBER: 60/085338
;; PRIOR FILING DATE: 1998-05-13
;; PRIOR APPLICATION NUMBER: 60/085339
;; PRIOR FILING DATE: 1998-05-13
;; PRIOR APPLICATION NUMBER: 60/085579
;; PRIOR FILING DATE: 1998-05-15

;; PRIOR APPLICATION NUMBER: 60/085697
;; PRIOR FILING DATE: 1998-05-15
;; PRIOR APPLICATION NUMBER: 60/085704
;; PRIOR FILING DATE: 1998-05-15
;; PRIOR APPLICATION NUMBER: 60/086414
;; PRIOR FILING DATE: 1998-05-22
;; PRIOR APPLICATION NUMBER: 60/086430
;; PRIOR FILING DATE: 1998-05-22
;; PRIOR APPLICATION NUMBER: 60/087106
;; PRIOR FILING DATE: 1998-05-28
;; PRIOR APPLICATION NUMBER: 60/088026
;; PRIOR FILING DATE: 1998-06-04
;; PRIOR APPLICATION NUMBER: 60/088730
;; PRIOR FILING DATE: 1998-06-10
;; PRIOR APPLICATION NUMBER: 60/088741
;; PRIOR FILING DATE: 1998-06-10
;; PRIOR APPLICATION NUMBER: 60/088810
;; PRIOR FILING DATE: 1998-06-10
;; PRIOR APPLICATION NUMBER: 60/088858
;; PRIOR FILING DATE: 1998-06-11
;; PRIOR APPLICATION NUMBER: 60/089532
;; PRIOR FILING DATE: 1998-06-17
;; PRIOR APPLICATION NUMBER: 60/089599
;; PRIOR FILING DATE: 1998-06-17
;; PRIOR APPLICATION NUMBER: 60/089907
;; PRIOR FILING DATE: 1998-06-18
;; PRIOR APPLICATION NUMBER: 60/089947
;; PRIOR FILING DATE: 1998-06-19
;; PRIOR APPLICATION NUMBER: 60/090349
;; PRIOR FILING DATE: 1998-06-23
;; PRIOR APPLICATION NUMBER: 60/090429
;; PRIOR FILING DATE: 1998-06-24
;; PRIOR APPLICATION NUMBER: 60/090445
;; PRIOR FILING DATE: 1998-06-24
;; PRIOR APPLICATION NUMBER: 60/090538
;; PRIOR FILING DATE: 1998-06-24
;; PRIOR APPLICATION NUMBER: 60/090863
;; PRIOR FILING DATE: 1998-06-26
;; PRIOR APPLICATION NUMBER: 60/091360
;; PRIOR FILING DATE: 1998-07-01
;; PRIOR APPLICATION NUMBER: 60/091519
;; PRIOR FILING DATE: 1998-07-02
;; PRIOR APPLICATION NUMBER: 60/091982
;; PRIOR FILING DATE: 1998-07-07

Query Match 6.1%, Score 39.8; DB 9; length 1377;
Best local similarity 56.5%; Pred. No. 0.17;
Matches 74; Conservative 0; Mismatches 57; Indels 0; Gaps 0;

Qy 37 CTGCTGCTGCCCCCGGCGCCCTTGCGCCCTTGAGGCCCCCAAGCTTCTGCTGCTG 96
Db 479 TTCTCCGCGGGCGGGGCTCCGAGGTCCCGGAGTCCCGGCTCCCGGCTTGCCTT 420
Qy 97 TGATCCCCCAGCGCGGCGGCGGCGGCGGCTCCGCGGCGGCGGCGGCGGCGGCGG 156
Db 419 TCTCTCCCGGAGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 360
Qy 157 CCGGCTTGCA 167
Db 359 CCGGCTTGCA 349

RESULT 10
US-10-121-049-361/C
; Sequence 361, Application US/10121049
; Publication No. US2003002239A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang

```

1  APPLICANT: Gerlitsen, Mary E.
2  APPLICANT: Goddard, Audrey
3  APPLICANT: Godowski, Paul J.
4  APPLICANT: Gurney, Austin L.
5  APPLICANT: Sherwood, Steven
6  APPLICANT: Smith, Victoria
7  APPLICANT: Stewart, Timothy A.
8  APPLICANT: Tuman, Daniel
9  APPLICANT: Matanabe, Collin K
10 APPLICANT: Wood, William
11 APPLICANT: Zhang, Zemin
12 TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
13 TITLE OF INVENTION: ACIDS ENCODING THE SAME
14 FILE REFERENCE: P3330R1C17
15 CURRENT APPLICATION NUMBER: US/10/121, 049
16 CURRENT FILING DATE: 2002-04-12
17 PRIOR Application removed - See File Wrapper or Palm
18 NUMBER OF SEQ ID NOS: 550
19 SEQ ID NO 361
20 LENGTH: 1377
21 TYPE: DNA
22 ORGANISM: Homo Sapien
23 US-10-121-049-361

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Query Match	6.1%	Score 39.8	DB 9	Length 1377
Best Local Similarity	56.5%	Pred No. 0.17		
Matches 74	Conservative 0	Mismatches 57	Indels 0	Gaps 0

Oy	37	CCTGCGCGGTGCACCCGGGGCCCCCTCTGGGCCCTTTAAGGCCGCCCAAGCTTTCGCGATGCTG	96
Db	419	CTCCTCGGGGGCCGGGGGTCCCCTCGAAGTCCCGGCAATGCCGGCCTCCCGCCCTCGCGCTT	420
Oy	97	TGAATCCCCCAAGCCGGGGACAAGGCCCCGCTCGCGTGGCCCGGTGGTGACCACAGGCC	156
Dd	419	TCTCTCCGGAGACCCCGGGCGCGCGCTGCGCGGCAATCGCGGCCGGGCAAGC	360
Oy	157	CCCGGTTGCCA	167
Dd	359	CTTGCTGCTGCCA	349

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RESULT 11
: US-10-123-904-361/C
: Sequence 361, Application US/10123904
: Publication No. US20030022328A1
: GENERAL INFORMATION:
: APPLICANT: Baker, Kevin P.
: APPLICANT: Beresini, Maureen
: APPLICANT: DeForge, Laura
: APPLICANT: Desnoyers, Luc
: APPLICANT: Filvaroff, Ellen
: APPLICANT: Geo, Mel-Olang
: APPLICANT: Gerritsen, Mary E.
: APPLICANT: Goddard, Audrey
: APPLICANT: Godowski, Paul J.
: APPLICANT: Gurney, Austin L.
: APPLICANT: Sherwood, Steven
: APPLICANT: Smith, Victoria
: APPLICANT: Stewart, Timothy A.
: APPLICANT: Tumas, Daniel
: APPLICANT: Watanabe, Colin K
: APPLICANT: Wood, William
: APPLICANT: Zhang, Zhenli
: TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
: FILE OF INVENTION: ACIDS ENCODING THE SAME
: FILE REFERENCE: P330R1C54
: CURRENT APPLICATION NUMBER: US/10/123,904
: CURRENT FILING DATE: 2002-04-16
: Prior Application removed - See file wrapper or palm
: NUMBER OF SEQ ID NOS: 550
: SEQ ID NO 361
: LENGTH: 1377
: TYPE: DNA

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[illegible]

RESULT 12
US-10-140-470-361/c
; Sequence 361, Application US/10140470
; Publication No. US20030022331A1

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GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Beresini, Maureen
APPLICANT: Deforge, Laura
APPLICANT: Desnoyers, Luc
APPLICANT: Filvaroff, Ellen
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerltsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Sherwood, Steven
APPLICANT: Smith, Victoria
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Collin K
APPLICANT: Wood, William
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P330R1C160
CURRENT APPLICATION NUMBER: US/10/140,470
CURRENT FILING DATE: 2002-05-06
Prior Application removed - See Palm or File Wrapper
NUMBER OF SEQ ID NOS: 350
SEQ ID NO 361
LENGTH: 1377
TYPE: DNA
ORGANISM: Homo Sapien
US-10-140-470-361

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	Query Match	6.1%;	Score 39.8;	DB 9,	Length 1377;	
	Best Local Similarity	56.5%;	Pred. No.0.17;			
Matches	74;	Conservative	0;	Mismatches	57;	Indels 0; Gaps 0.
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Db	479 CTCCTGTGGCGCCCGGGGGTCCCTCTGAGGTCGCGGAGATGCCGCGCTCCGCGCTTGCTTT	420				
OY	97 TGAATCCCCAAGCCGCGACGAGCGCCCGCATCCGCTGCGCCCGGATGTGGTCCACAGGCC	156				
Db	419 TCTCTCCCGGAGCCCGCGGGCGCGGTGGCGGCGCTGGCGGCAATCGCGGCGCCGCAAGC	360				
OY	157 CCGCGGTGCACA	167				
Db	359 CCTGGCTGCACA	349				


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FILE REFERENCE: P2548pt1C1
CURRENT APPLICATION NUMBER: US/09/944,444
CURRENT FILING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: 09/866,028
PRIOR FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: 60/067,411
PRIOR FILING DATE: December 3, 1997
PRIOR APPLICATION NUMBER: 60/065,334
PRIOR FILING DATE: December 11, 1997
PRIOR APPLICATION NUMBER: 60/065335
PRIOR FILING DATE: December 11, 1997
PRIOR APPLICATION NUMBER: 60/065,278
PRIOR FILING DATE: December 11, 1997
PRIOR APPLICATION NUMBER: 60/065,425
PRIOR FILING DATE: December 12, 1997
PRIOR APPLICATION NUMBER: 60/065,656
PRIOR FILING DATE: December 16, 1997
PRIOR APPLICATION NUMBER: 60/065,654
PRIOR FILING DATE: December 16, 1997
PRIOR APPLICATION NUMBER: 60/065,702
PRIOR FILING DATE: December 16, 1997
PRIOR APPLICATION NUMBER: 60/065,870
PRIOR FILING DATE: December 17, 1997
PRIOR APPLICATION NUMBER: 60/065,873
PRIOR FILING DATE: December 17, 1997
PRIOR APPLICATION NUMBER: 60/066,017
PRIOR FILING DATE: December 18, 1997
PRIOR APPLICATION NUMBER: 60/070,440
PRIOR FILING DATE: January 5, 1998
PRIOR APPLICATION NUMBER: 60/074,086
PRIOR FILING DATE: February 9, 1998
PRIOR APPLICATION NUMBER: 60/074,092
```

PRIOR APPLICATION NUMBER: 60/075,945
PRIOR FILING DATE: February 25, 1998
PRIOR APPLICATION NUMBER: 60/112,850
PRIOR FILING DATE: December 16, 1998
PRIOR APPLICATION NUMBER: 60/113,296
PRIOR FILING DATE: December 22, 1998
PRIOR APPLICATION NUMBER: 60/146,222
PRIOR FILING DATE: July 28, 1999
PRIOR APPLICATION NUMBER: PCT/US98/19330
PRIOR FILING DATE: September 16, 1998
PRIOR APPLICATION NUMBER: PCT/US98/25108
PRIOR FILING DATE: December 1, 1998
PRIOR APPLICATION NUMBER: 09/216,021
PRIOR FILING DATE: December 16, 1998
PRIOR APPLICATION NUMBER: 09/218,517
PRIOR FILING DATE: December 22, 1998
PRIOR APPLICATION NUMBER: 09/254,311
PRIOR FILING DATE: March 3, 1999
PRIOR APPLICATION NUMBER: PCT/US99/12252
PRIOR FILING DATE: June 22, 1999
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR FILING DATE: September 15, 1999
PRIOR APPLICATION NUMBER: PCT/US99/28409
PRIOR FILING DATE: NO. US2002/0102647A1eml
PRIOR APPLICATION NUMBER: PCT/US99/28313
PRIOR FILING DATE: NO. US2002/0102647A1eml
PRIOR APPLICATION NUMBER: PCT/US99/28301
PRIOR FILING DATE: December1, 1999
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR FILING DATE: December 16, 1999
PRIOR APPLICATION NUMBER: PCT/US00/03565
PRIOR FILING DATE: February 11, 2000
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: February 22, 2000
PRIOR APPLICATION NUMBER: PCT/US00/05841
PRIOR FILING DATE: March 2, 2000
PRIOR APPLICATION NUMBER: PCT/US00/08439
PRIOR FILING DATE: March 30, 2000
PRIOR APPLICATION NUMBER: PCT/US00/14042
PRIOR FILING DATE: May 22, 2000

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; PRIOR APPLICATION NUMBER: PCT/US00/20710
; PRIOR FILING DATE: July 28, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/32678
; PRIOR FILING DATE: December 1, 2000
; PRIOR APPLICATION NUMBER: PCT/US01/06520
; PRIOR FILING DATE: February 28, 2001
; NUMBER OF SEQ ID NOS: 120
; SEQ ID NO 41
; LENGTH: 1377
; TYPE: DNA
; ORGANISM: Homo Sapien
US-09-944-449-41

Query Match          6.1%; Score 39.8; DB 10; Length 1377;
Best Local Similarity 56.5%; Pred. No. 0.17;
Matches 74; Conservative 0; Mismatches 57; Indels 0; Gaps 0;

QY 37 CTCTGCGGCGCCCGCCCTCTGCGCCCTTGAGCGCCCGCCAGCTTGTGCTGCTG 96
DB 479 CTCTGCGGCGCCCGCCCGCCCTCTGAGGTCGCGGCGAGTCCGCGCTCCGCGCTT 420
QY 97 TGATCCCCCAGCGCGCGCGCGCGCTCGCGTGCCTGCGCGCGCGCGCGCGCGCC 156
DB 419 TCTCTCCCGAGACCCCGCGCGCGCGCGCTGCGGCGCTGCGGCGCATGCGCGCGCAAGC 360
QY 157 CCGCGTTGCCA 167
DB 359 CCTGCGTCCCA 349

RESULT 15
US-09-944-457-41/c
; Sequence 41, Application US/09944457
; Patent No. US20020110859A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Botstein, David
; APPLICANT: Baton, Dan
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gertsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Grimaldi, Paul
; APPLICANT: Gurney, Austin
; APPLICANT: Hillan, Kenneth
; APPLICANT: Kljavin, Ivar
; APPLICANT: Napier, Mary
; APPLICANT: Roy, Margaret
; APPLICANT: Tumas, Daniel
; APPLICANT: Wood, William
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P2548PICI
; CURRENT APPLICATION NUMBER: US/09/944,457
; CURRENT FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: 09/866,028
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/067,411
; PRIOR FILING DATE: December 3, 1997
; PRIOR APPLICATION NUMBER: 60/069,334
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069,335
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069,278
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069,425
; PRIOR FILING DATE: December 12, 1997
; PRIOR APPLICATION NUMBER: 60/069,696
; PRIOR FILING DATE: December 16, 1997
; PRIOR APPLICATION NUMBER: 60/069,694
; PRIOR FILING DATE: December 16, 1997
; PRIOR APPLICATION NUMBER: 60/069,702
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; PRIOR FILING DATE: December 16, 1997
; PRIOR APPLICATION NUMBER: 60/069,870
; PRIOR FILING DATE: December 17, 1997
; PRIOR APPLICATION NUMBER: 60/069,873
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; PRIOR APPLICATION NUMBER: 60/068,017
; PRIOR FILING DATE: December 18, 1997
; PRIOR APPLICATION NUMBER: 60/070,440
; PRIOR FILING DATE: January 5, 1998
; PRIOR APPLICATION NUMBER: 60/074,086
; PRIOR FILING DATE: February 9, 1998
; PRIOR APPLICATION NUMBER: 60/074,092
; PRIOR FILING DATE: February 9, 1998
; PRIOR APPLICATION NUMBER: 60/075,945
; PRIOR FILING DATE: February 25, 1998
; PRIOR APPLICATION NUMBER: 60/112,850
; PRIOR FILING DATE: December 16, 1998
; PRIOR APPLICATION NUMBER: 60/113,296
; PRIOR FILING DATE: December 22, 1998
; PRIOR APPLICATION NUMBER: 60/146,222
; PRIOR FILING DATE: July 28, 1999
; PRIOR APPLICATION NUMBER: PCT/US98/19330
; PRIOR FILING DATE: September 16, 1998
; PRIOR APPLICATION NUMBER: PCT/US98/25108
; PRIOR FILING DATE: December 1, 1998
; PRIOR APPLICATION NUMBER: 09/216,021
; PRIOR FILING DATE: December 16, 1998
; PRIOR APPLICATION NUMBER: 09/218,517
; PRIOR FILING DATE: December 22, 1998
; PRIOR APPLICATION NUMBER: 09/254,311
; PRIOR FILING DATE: March 3, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/12252
; PRIOR FILING DATE: June 22, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: September 15, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/28409
; PRIOR FILING DATE: No. US20020110859A1ember 30, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: No. US20020110859A1ember 30, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/28301
; PRIOR FILING DATE: December 1, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: December 16, 1999
; PRIOR APPLICATION NUMBER: PCT/US00/03565
; PRIOR FILING DATE: February 11, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: February 22, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/05841
; PRIOR FILING DATE: March 2, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/08439
; PRIOR FILING DATE: March 30, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/14042
; PRIOR FILING DATE: May 22, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/20710
; PRIOR FILING DATE: July 28, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/32678
; PRIOR FILING DATE: December 1, 2000
; PRIOR APPLICATION NUMBER: PCT/US01/06520
; PRIOR FILING DATE: February 28, 2001
; NUMBER OF SEQ ID NOS: 120
; SEQ ID NO 41
; LENGTH: 1377
; TYPE: DNA
; ORGANISM: Homo Sapien
US-09-944-457-41

Query Match          6.1%; Score 39.8; DB 10; Length 1377;
Best Local Similarity 56.5%; Pred. No. 0.17;
Matches 74; Conservative 0; Mismatches 57; Indels 0; Gaps 0;

QY 37 CTCTGCGGCGCCCGCCCTCTGCGCCCTTGAGCGCCCGCCAGCTTGTGCTGCTG 96
DB 479 CTCTGCGGCGCCCGCCCGCCCTCTGAGGTCGCGGCGAGTCCGCGCTCCGCGCTT 420
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GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: February 9, 2003, 18:46:59 : Search time 1931 Seconds
(without alignments)
5501.936 Million cell updates/sec

Title: US-10-060-066-2

Perfect score: 656

Sequence: 1 tatgcttcacactgcacact.....tgtaattttattctcttg 656

Scoring table: IDENTITY-NUC
Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues 32308132

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

EST :
1: em_estba:*
2: em_esthum:*
3: em_estlin:*
4: em_estlun:*
5: em_estlov:*
6: em_estlpl:*
7: em_estro:*
8: em_hlcc:*
9: gb_estcl:*
10: gb_estcl2:*
11: gb_hlcc:*
12: gb_estcl3:*
13: gb_estcl4:*
14: gb_estcl5:*
15: em_estclfun:*
16: em_estclom:*
17: gb_gsa:*
18: em_gsa_hum:*
19: em_gsa_luv:*
20: em_gsa_pin:*
21: em_gsa_vrt:*
22: em_gsa_fun:*
23: em_gsa_mam:*
24: em_gsa_mus:*
25: em_gsa_other:*
26: em_gsa_pro:*
27: em_gsa_rtd:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match Length	ID	Description
1	332.4	50.7	337	10	BE647856 UI-M-BH1-
2	234.2	35.7	558	14	BQ266161 NISC_f11
3	189.6	28.9	547	10	BE102334 UI-R-BT1-
4	174	26.5	245	12	BE864111 UI-M-BH1-
5	159.8	24.4	663	10	BB641732 BB641732
6	155.8	23.8	472	10	AM060348 UI-M-BH1-

7	102.2	15.6	983	17	CNS0489M	AL279005 Tetradon
8	86.4	13.2	600	12	BE803929	BG803929 0243-54 M
9	81.8	12.5	594	13	BE181765	BI981765 fu50d11.y
10	81.4	12.4	587	13	BI844628	BI844628 fq14g05.y
11	74.4	11.3	999	17	CNS04NDM	AL298579 Tetradon
12	73.6	11.2	691	13	BE912818	BE912818 602807258
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14	62	9.5	615	17	CNS04174	AL291865 Tetradon
15	61.4	9.4	687	17	CNS041QO	AL296459 Tetradon
16	61.4	9.4	688	10	BE212599	BE212599 IPbrn0032
17	61.4	9.4	697	10	BE574164	BE574164 IPbrn0116
18	56	8.5	923	17	CNS021DX	AL176675 Tetradon
19	54.4	8.3	575	17	FR0019451	AL012342 F_rubripe
20	54.4	8.3	580	10	BE222518	BE222518 hv92c08.x
21	54.4	8.3	599	9	AI912567	AI912567 w41b12.x
22	54.4	8.3	606	9	AI680925	AI680925 tx42h02.x
23	54.4	8.3	640	10	BE670632	BE670632 7e37e05.x
24	54	8.2	1043	17	CNS03MBE	AL250547 Tetradon
25	53.6	8.2	649	14	BM951619	BM951619 UI-M-EG0-
26	53.6	8.2	855	13	BI739481	BI739481 603361722
27	53.4	8.1	157	9	AI693801	AI693801 w487a03.x
28	53.4	8.1	965	13	BI457751	BI457751 603198193
29	52.8	8.0	477	12	BE861331	BE861331 UI-M-AK0-
30	52	7.9	739	13	BI553438	BI553438 603193385
31	52	7.9	757	13	BI821976	BI821976 603039793
32	52	7.9	763	13	BI753725	BI753725 603028241
33	52	7.9	776	12	BE705097	BE705097 602688041
34	52	7.9	788	13	BI546513	BI546513 603191523
35	52	7.9	872	13	BI821441	BI821441 603038325
36	52	7.9	890	13	BI544699	BI544699 603242658
37	52	7.9	1080	17	AO893056	AO893056 HS_4832.A
38	52	7.9	1938	11	BC033741	BC033741 Homo sapi
39	50.8	7.7	710	17	AO689558	AO689558 nbx0079L
40	50.4	7.7	436	17	B50198	B50198 C17978SK-89
41	49.8	7.6	776	17	CNS010RY	AL093932 Drosoph11
42	49.8	7.6	844	17	CNS0052P	AL056652 Drosoph11
43	49.8	7.6	887	14	BQ429511	BQ429511 AGENCOURT
44	49.8	7.6	971	17	AG079392	AG079392 pan trogl
45	49.6	7.6	641	9	AI357868	AI357868 qv13b02.x

ALIGNMENTS

RESULT 1
BE647856 337 bp mRNA linear EST 06-SEP-2000
UI-M-BH1-anh-c-12-0-UI.r1 NIH-BMAP.M.S2 Mus musculus cDNA clone
UI-M-BH1-anh-c-12-0-UI 5', mRNA sequence.

ACCESSION BE647856
VERSION BE647856.1 GI:9973676
KEYWORDS
SOURCE EST.
ORGANISM house mouse.
Mus musculus

REFERENCE
AUTHORS Bonaldo,M.F., Lennon,G. and Soares,M.B.
TITLE Normalization and subtraction: two approaches to facilitate gene discovery
JOURNAL Genome Res. 6 (9), 791-806 (1996)
MEDLINE 9704477

COMMENT

Contact: Chn, H
National Institute of Mental Health
6001 Executive Blvd. Room 7N-7190, MSC 9643, Bethesda, MD
20892-9643, USA
Tel: 301 443 1706
Fax: 301 443 9890
Email: mestr@mail.nih.gov
CDNA Library Preparation: M.B. Soares lab Clone distribution:
Researchers may obtain BMAP cDNA clones from RESEARCH GENETICS. It
should be noted that Bento Soares is generating a small number of
additional specialized non-redundant arrays of BMAP cDNAs whose

availability will be considered under appropriate and limited collaborative arrangements The following repetitive elements were found in this cDNA sequence: 88-148, >GC-rich#low_complexity
Seq primer: M13 Reverse.

FEATURES
source

Location/Qualifiers

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/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UI-M-BM1-anh-c-12-0-UI"
/clone_1lb="NIH_BMAP_M.S2"
/dev_stage="27-32 days"
/lab_host="DH10B (Life Technologies)"
/note="Vector: p773D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; The NIH_BMAP_M.S2 library is a subtracted library derived from NIH_BMAP_M.S1, which in turn is a subtracted library derived from a mixture of normalized libraries from ten regions of the mouse brain (cerebellum, brain stems, olfactory bulbs, hypothalamus, cortex, amygdala, basal ganglia, pineal gland, striatum, hippocampus). The driver used for subtraction consisted of a pool of 5,000 clones from the NIH_BMAP_M.S1 library and a pool of 2,000 clones obtained from non-normalized and normalized mouse brain spinal cord libraries."

BASE COUNT 56 a 128 c 86 g 67 t
ORIGIN

Query Match 50.7%; Score 332.4; DB 10; Length 337;
Best Local Similarity 99.7%; Pred. No. 1.6e-66;
Matches 333; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 17 ACCCTGCGCTGACGACCACTGCTGCTGCCCCCGCCCTTGGCCCTTGAAGGCC 76
DB 4 ACCCTGCGCTGACGACCACTGCTGCTGCCCCCGCCCTTGGCCCTTGAAGGCC 63
OY 77 CCCACTTCTGCTGTGCTGTATCCCGACAGCCGCGCCGCTCGCTGCC 136
DB 64 CCCACTTCTGCTGTGCTGTATCCCGACAGCCGCGCCGCTCGCTGCC 123
OY 137 CCGGTGAGTGGCCACGAGCCCGCGGTGCAAGTGAAGAGTGAAGAGCTG 196
DB 124 CCGGTGAGTGGCCACGAGCCCGCGGTGCAAGTGAAGAGTGAAGAGCTG 183
OY 197 GATGAAGAGAGGGGTTGTGTGTGAAGAGGGCTTCACTGATGACCACTCGG 256
DB 184 GATGAAGAGAGGGGTTGTGTGTGAAGAGGGCTTCACTGATGACCACTCGG 243
OY 257 CCGCTTGGCGGCTTTGGCTCATGACCTGCGCATGACTGACTGCTACAC 316
DB 244 CCGCTTGGCGGCTTTGGCTCATGACCTGCGCATGACTGACTGCTACAC 303
OY 317 AAGAGCTCATGTCGACACCAACCACTCACA 350
DB 304 AAGAGCTCATGTCGACACCAACCACTCACA 337

RESULT 2
LOCUS B0266161 558 bp mRNA linear EST 07-MAY-2002
DEFINITION NISC_ff11c05.x1 NCI_CGAP_Mam5 Mus musculus cDNA clone IMAGE:2865416
ACCESSION B0266161
VERSION B0266161.1 GI:20491226
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 558)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index

JOURNAL
COMMENT

Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgabs-remail.nih.gov
Tissue Procurement: Lothar Hennighausen/Robin Humphreys
CDNA Library Preparation: Life Technologies
CDNA Library Arrayed by: The I.M.A.G.E. Consortium/LLNL
DNA Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC)
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
info@image.llnl.gov
NCI:1046188
Plate: LAM7069 row: F column: 9
Seq primer: -21M13 forward primer (ABI).

FEATURES
source

Location/Qualifiers

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/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="IMAGE:2865416"
/clone_1lb="NCI_CGAP_Mam5"
/tissue_type="tumor, gross tissue"
/dev_stage="7 months"
/lab_host="DH10B"
/note="Organ: mammary; Vector: pCMV-SPORT6; Site_1: SalI; Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT. Library constructed by Life Technologies. Investigators providing samples: Lothar Hennighausen/Robin Humphreys, NIH"

BASE COUNT 153 a 152 c 131 g 122 t
ORIGIN

Query Match 35.7%; Score 234.2; DB 14; Length 558;
Best Local Similarity 89.2%; Pred. No. 6.9e-44;
Matches 256; Conservative 0; Mismatches 30; Indels 1; Gaps 1;

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DB 558 CCCATCGTGGGGGCGAGTGGCTCTCCGAGAGAGAGACCTGGGGGCTCACATTAG 499
OY 430 GCGTGTGGCGGATATGCTGCGCTGGAAGGTAGAGGTGACGAGAGCCCTGGCCACCTC 489
DB 488 GCGTGTGGCGGATATGCTGCGCTGGAAGGTAGAGGTGACGAGAGCCCTGGCCACCTC 439
OY 490 CGNTGAGCCGTGTGCTTCAGCAATTCAGTCTTATGTTCTGACTCTCAACCCAAAGNC 549
DB 438 CGCTGAGCCGTGTGCTTCAGCAATTCAGTCTTATGTTCTGACTCTCAACCCAAAGNC 379
OY 550 TTGAGGGGTGTGCTTACTGCTGGAGGGGAGTNTATTCATGACACCCCTCATNCTNT 609
DB 378 TTGATGGGTGTGCTTACTGCTGGAGGGGAGTNTATTCATGACACCCCTCATNCTNT 319
OY 610 ACAATCCCTCTTGGGGATTTNTGNTGTTATTTATTTTCTTGTG 656
DB 318 -CAATCCCTCTTGGGATTCGCTTTATTTATTTATTTACTGG 273

RESULT 3
LOCUS BE102334 547 bp mRNA linear EST 13-JUN-2000
DEFINITION UT-R-BT1-aql-d-02-0-UI.s1 UT-R-BT1 Rattus norvegicus cDNA clone
ACCESSION BE102334
VERSION BE102334.1 GI:8494433
KEYWORDS EST.
SOURCE Norway rat.
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

REFERENCE 1 (bases 1 to 547)
AUTHORS Bonaldo,M.F., Lennon,G. and Soares,M.B.
TITLE Normalization and subtraction: two approaches to facilitate gene

JOURNAL
MEDLINE
COMMENT

discovery
Genome Res. 6 (9), 791-806 (1996)
97044477
Contact: Soares, MB
Program for Rat Gene Discovery and Mapping
University of Iowa
451 Eckstein Medical Research Building Iowa City, IA 52242, USA
Tel: 319 335 8250
Fax: 319 335 9565
Email: msoares@blue.weeg.uiowa.edu

The sequence contained an oligo-dT track that was present in the oligonucleotide that was used to prime the synthesis of first strand cDNA and therefore this may represent a bonafide poly A tail. The sequence tag present in the cDNA between the NotI site and the oligo-dT track served to identify it as a clone from the normalized corpus striatum library cDNA Library Preparation: M.B. Soares Lab Clone distribution: clones will be available through Research Genetics (www.resgen.com) The following repetitive elements were found in this cDNA sequence: 147-294, >B3SINE/B2
Seq primer: M13 Forward
POLYA=yes.

FEATURES
SOURCE

Location/Qualifiers
1. 347
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/strain="Sprague-Dawley"
/db.xref="taxon:10116"
/clone="ur-R-BT1-aq1-d-02-0-UI"
/clone_lib="ur-R-BT1"
/dev_stage="adult"
/lab_host="DH10B (Life Technologies)"
/note="Vector: pT73D-Pac (Pharmacia) with a modified polylinker: Site.1: Not I; Site.2: Eco RI; The library ur-R-BT1 is a subtracted library derived from a mixture of the following tissues: hippocampus, thalamus, mid-brain, medulla, corpus striatum, cerebral cortex and testis. For a detailed description of the library from which this clone was derived, please visit our web site at retest.eng.uiowa.edu. The subtraction has been previously described in (Bonaldo, Lennon and Soares, Genome Research 6:791-806, 1996)
TAG_LIB=ur-R-BT1
TAG_TISSUE=corpus-striatum
TAG_SEQ=CTAGG"

BASE COUNT 150 a 148 c 121 g 128 t

ORIGIN

Query Match 28.9%; Score 189.6; DB 10; Length 547;
Best Local Similarity 90.5%; Pred. No. 1.3e-33;
Matches 209; Conservative 0; Mismatches 21; Indels 1; Gaps 1;

QY 375 CGTGGGGGCACTGCTCTCCGAGAGAGAGACCTGGGGGCTCACACATTTCAGGCTC 434
|||||
Db 547 CGTGGGGGCACTGCTCTCCGAGAGAGAGACCTGGGGGCTCACACATTTCAGGCTC 488
|||||
QY 435 TGGGGGATATGCTGCTGGAAGGTAGGGTGAGAGAGCCCTGGCTGGCCACCTCCGTTG 494
|||||
Db 487 TGGGGATATGCTGCTGGAAGGTAGGGTGAGAGAGCCCGAGCTGCCCTCCGCTG 428
|||||
QY 495 AACCTGTGCTTCAGCAATCGACTTNTAGTCTTCAGAGTCTCAACCAAGAGCTTGAG 554
|||||
Db 427 AAGCTGTGCTTCAGCAAGCAAGCACTGCTATGTTCTGAATCTATCCCAAGGCTTTGAG 368
|||||
QY 555 GGGTGTGCTTACTGCTGAGAGCG-GTNTNATTCATGACCCCTCCATTGCC 604
|||||
Db 367 GGGTGTGCTTACTGCTGAGAGCGCTATGATTCATGATCCCTCTGTGCC 317
|||||

RESULT 4
BE864111/c 245 bp mRNA linear EST 29-SEP-2000
LOCUS BE864111
DEFINITION UI-M-BH1-amp-a-08-0-UI.r1 NIH_BMAP_M_S2 Mus musculus cDNA clone
UI-M-BH1-amp-a-08-0-UI 5', mRNA sequence.
ACCESSION BE864111

VERSION
KEYWORDS
SOURCE
ORGANISM

BE864111.1 GI:10384829
EST.
house mouse.
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Scuriognathi; Muridae; Murinae; Mus.
1 (bases 1 to 245)
Bonaldo, M.F., Lennon, G. and Soares, M.B.
Normalization and subtraction: two approaches to facilitate gene
discovery
Genome Res. 6 (9), 791-806 (1996)
97044477
Contact: Chin, H
National Institute of Mental Health
6001 Executive Blvd. Room 7N-7190, MSC 9643, Bethesda, MD
20892-9643, USA
Tel: 301 443 1706
Fax: 301 443 9890
Email: m3st@mail.nih.gov

REFERENCE
AUTHORS
TITLE
JOURNAL
MEDLINE
COMMENT

Researchers may obtain BMAP cDNA clones from RESEARCH GENETICS. It should be noted that Bento Soares is generating a small number of additional specialized non-redundant arrays of BMAP cDNAs whose availability will be considered under appropriate and limited collaborative arrangements
Seq primer: M13 Reverse.

FEATURES
SOURCE

Location/Qualifiers
1. 245
/organism="Mus musculus"
/strain="C57BL/6J"
/db.xref="taxon:10090"
/clone="ur-M-BH1-amp-a-08-0-UI"
/clone_lib="NIH_BMAP_M_S2"
/dev_stage="27-32 days"
/lab_host="DH10B (Life Technologies)"
/note="Vector: pT73D-Pac (Pharmacia) with a modified polylinker: Site.1: Not I; Site.2: Eco RI; The NIH_BMAP_M_S2 library is a subtracted library derived from NIH_BMAP_M_S1, which in turn is a subtracted library derived from a mixture of normalized libraries from ten regions of the mouse brain (cerebellum, brain stems, olfactory bulbs, hypothalamus, cortex, amygdala, basal ganglia, pineal gland, striatum, hippocampus). The driver used for subtraction consisted of a pool of 5,000 clones from the NIH_BMAP_M_S1 library and a pool of 2,000 clones obtained from non-normalized and normalized mouse brain spinal cord libraries."

BASE COUNT 39 a 67 c 77 g 61 t 1 others

ORIGIN

Query Match 26.5%; Score 174; DB 12; Length 245;
Best Local Similarity 99.4%; Pred. No. 5.3e-30;
Matches 174; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 283 CCATCGCATAGACGACGACTACTGCTCTACACAAAGCTCTCATCTGCACACACCA 342
|||||
Db 245 CCATCGCATAGACGACGACTACTGCTCTACACAAAGCTCTCATCTGCACACCA 186
|||||
QY 343 ACCCTACAGCAGGATGATGACGACACCCCATCTGGGGGAGAGTGGCTCCGAGAAGA 402
|||||
Db 185 ACCCTACAGCAGGATGATGACGACACCCCATCTGGGGGAGAGTGGCTCCGAGAAGA 126
|||||
QY 403 AGAACCTGGGGGCTTCACACATTGAGGCTCTGGGGGATVGGCTGCTGGAAG 457
|||||
Db 125 AGAACCTGGGGGCTTCACACATTGAGGCTCTGGGGGATVGGCTGCTGGAAG 71
|||||

RESULT 5
BB641732 663 bp mRNA linear EST 26-OCT-2001
LOCUS BB641732
DEFINITION BB641732 RIKEN full-length enriched, 10 days neonate cortex Mus
musculus cDNA clone AB30045A22 5', mRNA sequence.
ACCESSION BB641732

VERSION	KEYWORDS	SOURCE	ORGANISM	REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
BB641732.1	GI:16476827	house mouse.	house mouse.	EST.				
		Mus musculus	Mus musculus	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
		1 (bases 1 to 663)						
		Arakawa,T., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hiramoto,K., Hori,F., Ishii,Y., Ito,M., Kawai,T., Kono,H., Kouda,M., Koyu,S., Matsuyama,T., Miyazaki,A., Nomura,K., Ohno,M., Okazaki,Y., Okido,T., Saito,R., Sakai,C., Sakai,K., Sano,H., Sasaki,D., Shibata,K., Shingawa,A., Shiraki,T., Sogabe,Y., Suzuki,H., Tagami,M., Tagawa,A., Takahashi,F., Takeda,Y., Tanaka,T., Toya,T., Muramatsu,M. and Hayashizaki,Y.						
		RIKEN Mouse ESTs (Arakawa,T., et al. 2001)						
		Unpublished (2001)						
		Contact: Yoshihide Hayashizaki						
		Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute						
		The Institute of Physical and Chemical Research (RIKEN)						
		1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan						
		Tel: 81-45-503-9222						
		Fax: 81-45-503-9216						
		Email: genome-res@gsic.riken.go.jp,						
		URL: http://genome.gsc.riken.go.jp/						
		Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Kono,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.						
		Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)						
		wag1,K., Fujiwaka,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Matshiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,T., Okazaki,Y., Muramatsu,M., Inoue,Y., Kiria,A. and Hayashizaki,Y.						
		RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)						
		Kono,H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P., Sugahara,Y. and Hayashizaki,Y.						
		Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)						
		Kondo,S., Shingawa,A., Saito,T., Kiyosawa,H., Yamanaka,I., Aizawa,K., Fukuda,S., Hara,A., Itoh,M., Kawai,J., Shibata,K. and Hayashizaki,Y.						
		Computational Analysis of Full-length Mouse cDNAs Compared with Human Genome Sequences. Mamm. Genome. 12, 673-677 (2001)						
		Please visit our web site (http://genome.gsc.riken.go.jp) for further details.						
		e mouse tissues.						
		Location/Qualifiers						
		1. .663						
		/organism="Mus musculus"						
		/db_xref="taxon:10090"						
		/clone="AB30045A22"						
		/clone_lib="RIKEN full-length enriched, 10 days neonate cortex"						
		/tissue_type="cortex"						
		/dev_stage="10 days neonate"						
		/lab_host="DH10B"						
		/note="Site_1: Sali; Site_2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5'						
		GAGGAGAGAGAGATCCAGAGAGCTCTTTTCTTTTCTTTTCTTTVN 3']						
		cDNA was prepared by using trehalase thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. cDNA went through one round of normalization						
		to Rot = 20.0 and subtraction to Rot = 459.0. Second						
		strand cDNA was prepared with the primer adapter of						

BASE COUNT	88 a	236 c	142 g	197 t
ORIGIN				
Query Match	24.4%	Score 159.8;	DB 10;	Length 663;
Matches Local Similarity	80.6%	Pred. No. 9.6e-27;		
Batches 199; Conservative	0;	Mismatches 47;	Indels 1;	Gaps 1;

```

sequence [5' GAGAGAGAATTCGAGTTAAATTAATCCCGCCCCCCC
3']. cDNA was cleaved with XhoI and BamHI. Vector: a
modified pBluescript KS(+) after bulk excision from lambda
FLC 1.

```

QY	1	TATGGCTTCACTGCACACTTCGCTTCGACGCCACCTGTCTGCGTCCCGCCCCCTC	60
Db	409	TATGGCTTACTCTG-ACTTTGGCTATGCAGCCACCTGCTGGTGCCACAGGCACTC	467
QY	61	TGGCCCTTGAGGCCCCCGACCTTCTGCTGTGATCCCCAGCGCCGACGG	120
Db	468	TGGCTCTTGAGGCCCCCGACCTTCTGTGTAGCTGTGATACCACCGCTCTGCACGG	527
QY	121	CCCGCCCTCCGCTCCCGGCGTGCGGCCACAGGCCCCCGGTTGCGCATGTGAATCG	180
Db	528	CCCGCCCTCTCTCCCGCGGTGGGCCACAGGCTCCCGGCGCATTTGGCGAATCG	587
QY	181	AGTCATTGAACGCTGGAATGAGAGAGGGGTTTTGTGTGAAAAGGCGCTTCAGTAC	240
Db	588	AGTCATGTAACCCCGTATGAAATGAGAGATGTGCTGTACAGCTTTTATCGCT	647
QY	241	TACTGAC	247
Db	648	TCCCGAC	654

RESULT 6
AM060348/c LOCOS
DEFINITION
UT-M-BH1-anh-c-12-0-UI.s1 NIH BMAP_M_52 Mus musculus cDNA clone
UT-M-BH1-anh-c-12-0-UI 3', mRNA sequence.
ACCESSION AM060348
VERSION AM060348.1 GI:608099
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 472)
AUTHORS Bonaldo,M.F., Lennon,G. and Soares,M.B.
TITLE Normalization and subtraction: two approaches to facilitate gene discovery
JOURNAL Genome Res. 6 (9), 791-806 (1996)

JOURNAL MEDLINE
COMMENT 97044477
Contact: Chin, H
National Institute of Mental Health
6001 Executive Blvd. Room 7N-7190, MSC 9643, Bethesda, MD
20892-9643, USA
Tel: 301 443 1706
Fax: 301 443 9890
Email: mstemail.nih.gov
The sequence contained an oligo-dT track that was present in the
oligonucleotide that was used to prime the synthesis of first
strand cDNA and therefore this may represent a bonafide poly A
tail. The sequence tag present in the cDNA between the NotI site
and the oligo-dT track served to identify it as a clone from the
normalized hypochalamos library cDNA Library Preparation: M.B.
Soares Lab Clone Distribution: NIH BMAP cDNA clones will be made
available by the means that is soon to be determined. When NIH
determines the means for distribution of the BMAP cDNA clones, this
record will be updated accordingly when that means is determined.
The following repetitive elements were found in this cDNA sequence:
150-287, >B3#SINE/B2
Seq primer: M13 Forward
POLYA=Yes.

FEATURES
source location/Qualifiers
1..472

Query Match	23.8%;	Score 155.8;	DB 10;	Length 472;
Best Local Similarity	85.5%;	Pred. No. 8.1e-26;		
Matches 177; Conservative	0;	Mismatches 29;	Indels 1;	Gaps 1;

293 TCTCCGTTTATTATTATTACTCG 267

DEFINITION Tetraodon nigroviridis genome survey sequence T7 end of clone

ORGANISM

TITLE

source

ORIGIN

0 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 37 38 39 40 41 42 43 44 45 46 47 48 49 50 51 52 53 54 55 56 57 58 59 60 61 62 63 64 65 66 67 68 69 70 71 72 73 74 75 76 77 78 79 80 81 82 83 84 85 86 87 88 89 90 91 92 93 94 95 96 97 98 99

DD 400 MAGCAGAGAGG

1
2
3
4
5
6
7
8

100

COMMENT

50

/organism="Mus musculus"

BASE COUNT	108 a	208 c	182 g	102 t	
ORIGIN					
Query Match	13.2%	Score 86.4;	DB 12;	Length 600;	
Best Local Similarity	66.8%;	Pred. No. 7.9e-10;			
Matches 123;	Conservative 0;	Mismatches 61;	Indels 0;	Gaps 0;	
<p>/db_xref="taxon:10090" /clone_lib="Mouse E14.5 retina lambda ZAP II library" /tissue_type="neural retina" /dev_stage="embryonic day 14.5 post-fertilization" /note="Vector: pAMP10 (Gibco); Cloned unidirectionally. Primer: Oligo dT. RNA Isolation: cytoplasmic RNA preps (Mannatis); Cloning Technique: cDNA Cloning (Clontech, Life Technologies); Average insert size: 1.8 kb; Insertion site: TACGTCACGATTCGAGG-->. Other information regarding entire library may be found at http://pga.su.med.edu/Data/libraries/microarray_cdna_library ies.htm."</p>					
Oy	214	TGTGTTGGAAGAAGGGCTTCAGCTACACACCATGGGCCCTTTCGGCTTTG	273		
Db	91	TGCGATGGGACCGCGGGGTGCAGATGCTGTGACACGCGGACCTTCGGCGGCTCT	150		
*Oy	274	GCGCTATACCATCGCATCGCATGACACTGACTGTGCTGTACACAGAGCTCATCTGCA	333		
Db	151	CGCTATATGGCATCTGCCCATCGCACCGACTACTGGCTGTACTCCAGCGCGCATCTGCA	210		
Oy	334	ACAGCAGCAACCTCAGACGAGGTATGACGAGCACCCCATGCTGGGGGCACTGGCTCT	393		
Db	211	ACGGCAGCAACCTGACATGTGACGACGGGCCCGCCCGCGGCTGTGGCGCGACATCA	270		
Oy	394	CCGA 397			
Db	271	CCCA 274			
RESULT 9					
LOCUS	BI981765	594 bp	mRNA	linear	EST 26-JUL-2002
DEFINITION	fu50d11.1 zebrafish adult brain Danio rerio cDNA clone 5333036 5'				
	similar to TR:Q9UGZ7 Q9UGZ7 DJ29316.1 ; mRNA sequence.				
ACCESSION	BI981765				
VERSION	BI981765.1	GI:16370697			
KEYWORDS	EST.				
SOURCE	zebrafish.				
ORGANISM	Danio rerio.				
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes; Cyprinidae; Danio.				
REFERENCE	1 (bases 1 to 594) Clark,M., Johnson,S.L., Lehrach,H., Lee,R., Li,F., Marra,M., Eddy ,S., Hillier,L., Kucab,T., Martin,D., Beck,C., Wylie,T., Underwood ,R., Stepoe,M., Theising,B., Allen,M., Bowers,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ritter,E., Kohn,S., Shih,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R. and Wilson,R.				
AUTHORS	Washu zebrafish EST Project 1998				
	Unpublished (1998)				
TITLE	Other ESTs: fu50d11.x1				
JOURNAL	Contact: Stephen L. Johnson				
COMMENT	Washington University School of Medicine 444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA Tel: 314 286 1800 Fax: 314 286 1810 Email: zbrfish@watson.wustl.edu cDNA Library Preparation: John Ngai. cDNA Library Arrayed by: Matthew Clark. DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: Genome Systems, St. Louis, Missouri (web address: www.genomesystems.com) (email contact: info@genomesystems.com) and Research Genetics, Huntsville, Alabama (web address: www.resgen.com) (email contact: info@resgen.com) and ResourcenetZentrumPrimaDatenbank, Berlin, Germany (web address: www.rzp.de)				

FEATURES	source	Seq primer: T7	High quality sequence stop: 438.
ORGANISM	Danio rerio	Location/Qualifiers	
REFERENCE	1. 594		
AUTHORS	/db_xref="taxon:7955"		
	/clone="5333036"		
	/clone_lib="zebrafish adult brain"		
	/sex="mixed male and female"		
	/tissue_type="brain"		
	/dev_stage="adult"		
	/lab_host="E. coli DH10B"		
	/note="Vector: pZiPlox; site_1: NotI; site_2: SalI; original library was constructed in lambdaZiPlox. Mass excision of the cDNA library was performed to yield pZiPlox plasmids. Insert check was done in original library."		
BASE COUNT	167 a 136 c 147 g 144 t		
ORIGIN			
Query Match	12.5%; Score 81.6; DB 13; Length 594;		
Best Local Similarity	67.1%; Pred. No. 9.1e-09;		
Matches 116; Conservative	0; Mismatches 57; Indels 0; Gaps 0;		
QY	186 TTGAACCCCTGAGAGAGAGAGGGCTTTGGCTGTGAAGAGCGCTCAGTACTACTG 245		
Db	421 TTGAAGGACACAAACCTCGCCCTGACGGATGGTGTGTGAAGAGCATTCACATCTCTC 480		
QY	246 ACCACCATCGCGCGCTTCGCGCGCTTTGGAGCTCATGACCATCGCATCAGCATGACTAC 305		
Db	481 ACCATCGGGGTGCATTCGCATCTTTGGCTGTGATGACGGTGGCTATCGCATGATTAC 540		
QY	306 TGGCTTACACAGAGCTCTCATCTGACACACCAACCTCAGACAGGTGA 358		
Db	541 TGGCTTACTCGCGCGCTCATCTGACACAGACCGCCACACACACACAGA 593		
RESULT 10			
LOCUS	BI844628		
DEFINITION	BI844628 587 bp mRNA linear EST 26-JUL-2002		
ACCESSION	BI844628		
VERSION	BI844628.1		
KEYWORDS	EST.		
SOURCE	zebrafish.		
ORGANISM	Danio rerio		
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
	Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes		
	; Cyprinidae; Danio.		
	1 (bases 1 to 587)		
	Clark,M., Johnson,S.L., Lehrach,H., Lee,R., Li,F., Maria,M., Eddy		
	,S., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T., Underwood		
	,R., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person,B.,		
	Swaller,J., Gibbons,M., Page,D., Harvey,N., Schuck,R., Ritter,E.,		
	Kohn,S., Shih,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R.		
	and Wilson,R.		
	Mashu zebrafish EST Project 1998		
	Unpublished (1998)		
	Contact: Stephen L. Johnson		
	Washington University School of Medicine		
	4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA		
	Tel: 314 286 1800		
	Fax: 314 286 1810		
	Email: zbrafish@wustl.edu		
	cDNA Library Preparation: John Ngai. cDNA Library Arrayed by:		
	Matthew Clark. DNA Sequencing by: Washington University Genome		
	Sequencing Center Clone distribution by: Genome Systems, St. Louis,		
	Missouri (web address: www.genomesystems.com) (email contact:		
	info@genomesystems.com) and Research Genetics, Huntsville, Alabama		
	(web address: www.resgen.com) (email contact: info@resgen.com) and		
	Ressourcenzentrum Primardatenbank, Berlin, Germany (web address:		
	www.tzpd.de)		
TITLE			
JOURNAL			
COMMENT			

ORIGIN	
Query Match	11.28; Score 73.6; DB 13; Length 691

Best Local Similarity 65.4%; Pred. No. 7e-07;		Matches 123; Conservative 0; Mismatches 64; Indels 1; Gaps 1;			
QY	211	GTTTGTGTGTAAGGCGCTTACGACTAGTACGACCATGCGCGCTTTCGGGCTT	270		
DB	4	GGTGTCTATGGACCGCGGCTGTCATGCTGTCGACACGCGCGAGCTTTCGGGCT	63		
QY	271	TTCGCTCATGACCATGCGCCATCAGACTGACTGCTTACACAGAGCTCTCATCT	330		
DB	64	TCTGCTCATGAGCCATTCGCCATCGCACCGACTGCTGATCTCCAGCGGACATCT	123		
QY	331	GCAAC-ACCACCAACCTTCACAGCAGTGTATGACGACACCCCATCGTGGGCGAGTGGC	389		
DB	124	GCACTGCACCAACCTTACCATGAGACGAGGCCCCCGCCCGCGCGGACATCT	183		
QY	390	TCTTCGGA 397			
DB	184	CTCACCCA 191			
RESULT 13					
LOCUS	FR0019468	592 bp	DNA linear GSS 10-DEC-1997		
DEFINITION	F.rubripes GSS sequence, clone 029J13bd4, genomic survey sequence.				
ACCESSION	AL012359	AL012359.1 GI:2678727			
VERSION	GSS: genome survey sequence.				
KEYWORDS	Takifugu rubripes				
SOURCE	Takifugu rubripes				
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Acanthopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes; Tetraodontidae; Takifugu.				
REFERENCE	1 (bases 1 to 592)				
AUTHORS	Elgar,G., Clark,M., Smith,S., Meek,S., Warner,S., Umranta,Y., Williams,G. and Brenner,S.				
TITLE	Direct Submission				
JOURNAL	Submitted (08-DEC-1997) MRC Human Genome Mapping Project Resource Centre Hinxton, Cambridge, CB10 1SB. Email: blh@hgmrc.mrc.ac.uk				
COMMENT	Vector: pBluescript II KS V.type: phagemid PRIMER: KS DESCR: One pass dye-terminator sequencing of cosmid cloned genomic sequence.				
FEATURES					
source					
1..592					
/organism="Takifugu rubripes"					
/db_xref="taxon:31033"					
/clone="029J13bd4"					
/clone_11b="cosmid 029J13"					
BASE COUNT 130 a 147 c 133 g 129 t 53 others					
ORIGIN					
Query Match 11.2%; Score 73.2; DB 17; Length 592;					
Best Local Similarity 69.2%; Pred. No. 8.7e-07;					
Matches 99; Conservative 0; Mismatches 44; Indels 0; Gaps 0;					
QY	216	TGTTGTGAAGGCGGTTCAGTACTAGTACGACCATCGGCGCTTCGGGCTTTGGC	275		
DB	86	TGTTGTGACCGCGGAGTTTCAACGCTGTTGGCGCAGTGGGGGCTTTCGGCGCTTCAGC	145		
QY	276	CTCATGACCATGCGCATGAGCTGACTGCTCTACACAAGAGCTCTCATCTGCAC	335		
DB	146	CTGATNACTATGCGCATTTGGCAGCGAGCTACTGCTCTATTCGGGCGGCTCATCTGCAT	205		
QY	336	ACCACCAACCTTCACAGCAGGTGA 358			
DB	206	ACCACCAATGCGCACCGAGCA 228			
RESULT 14					
RNS04174/c					

LOCUS	CNS04174	615 bp	DNA	linear	GSS 21-MAY-2000
DEFINITION	Tetraodon nigroviridis genome survey sequence T7 end of clone 111N04 of library G from Tetraodon nigroviridis, genomic survey sequence.				
ACCESSION	AL291865	GI:8030445			
VERSION	AL291865.1	GSS: genome survey sequence.			
KEYWORDS	GSS: genome survey sequence.				
SOURCE	Tetraodon nigroviridis				
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Acanthopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes; Tetraodontidae; Tetraodon.				
REFERENCE	1 (bases 1 to 615)				
AUTHORS	Roest-Crolius,H., Jallion,O., Dasilva,C., Bouneau,L., Fisher,C., Bernot,A., Fizesmes,C., Wincker,P., Brotier,P., Quetier,F., Saurin,W. and Weissbach,J.				
TITLE	Human gene number estimate provided by genome wide analysis using Tetraodon nigroviridis DNA sequence				
JOURNAL	Unpublished				
AUTHORS	2 (bases 1 to 615)				
REFERENCE	Roest-Crolius,H., Jallion,O., Dasilva,C., Fizesmes,C., Fisher,C., Bouneau,L., Billault,A., Quetier,F., Saurin,W., Bernot,A. and Weissbach,J.				
TITLE	Characterization and repeat analysis of the compact genome of the freshwater pufferfish Tetraodon nigroviridis				
JOURNAL	Unpublished				
AUTHORS	3 (bases 1 to 615)				
TITLE	Genoscope.				
JOURNAL	Direct Submission				
COMMENT	Submitted (12-APR-2000) This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetraodon .				
FEATURES	location/Qualifiers				
source	1..615				
	/organism="Tetraodon nigroviridis"				
	/db_xref="taxon:99883"				
	/clone="111N04"				
	/clone_11b="G"				
	/note="Genoscope sequence ID : C0B6111D02LP1-end : T7"				
BASE COUNT	130 a	162 c	187 g	130 t	6 others
ORIGIN					
Query Match	9.5%; Score 62; DB 17; Length 615;				
Best Local Similarity	63.3%; Pred. No. 0.00033;				
Matches	159; Conservative	2; Mismatches	78; Indels	12; Gaps	4;
QY	214	TGTGTTGTGAAAGGCGCTTCAGTACTAGTACCATCGGCGC-CTTCGCGGCTTT	272		
DB	341	TGTGTTGTGAGCGCGGCATCGTGTGCTCACCMCATGGGAGCTTTTGACACCTTC	282		
QY	273	GGCCTATGACCATCGGCATCAGA-CTGACTATGCGTCTACACAAGCTCTATCTG	331		
DB	281	GCCCTGATGACGGTGCATCGCATCGACTAGTGGCTGTGACGCTCGCGCTTATCTG	222		
QY	332	CACACCAACCACTCACAGCAGTATGATGACGACACCCCATCTGCGGCGAGTGGCTC	391		
DB	221	CACACAGA-CGGCCATCTCCACCTCAGAGCAGCTCCACAGCATCTATATAGTACA--	165		
QY	392	CTCCGAGAAGAAAGCCTCGGGGCTTCACACATTCAGGCTCTGCGGATATGCTGCT	451		
DB	164	-----AGAAAGACCTCGGGGCTTCACACATTCAGGCTCTGAGAGTTCGCTGCT	112		
QY	452	GGAAGTAGGG 462			
DB	111	GGTAGGTACGG 101			
RESULT 15					
CNS04100	CNS04100	687 bp	DNA	linear	GSS 21-MAY-2000

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